

<110> APPLICANT: Hardie, David Grahame
 Alessi, Dario
 Boudeau, Jerome
 <120> TITLE OF INVENTION: Methods For Use Of An LKB1/Strad7M025 Complex
 <130> FILE REFERENCE: 002.00270
 <140> CURRENT APPLICATION NUMBER: US/10/565,058
 <141> CURRENT FILING DATE: 2006-01-17
 <150> PRIOR APPLICATION NUMBER: PCT/GB2004/003096
 <151> PRIOR FILING DATE: 2004-07-16
 <150> PRIOR APPLICATION NUMBER: GB 0316725.1
 <151> PRIOR FILING DATE: 2003-07-17
 <150> PRIOR APPLICATION NUMBER: GB 0330078.7
 <151> PRIOR FILING DATE: 2003-12-20
 <160> NUMBER OF SEQ ID NOS: 159
 <170> SOFTWARE: PatentIn version 3.1

<210> SEQ ID NO 1
 <211> LENGTH: 550
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 1

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Met Ala Thr Ala Glu Lys Gln Lys His Asp Gly Arg Val Lys Ile Gly
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His Tyr Ile Leu Gly Asp Thr Leu Gly Val Gly Thr Phe Gly Lys Val
              20              25              30
Lys Val Gly Lys His Glu Leu Thr Gly His Lys Val Ala Val Lys Ile
              35              40              45
Leu Asn Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Arg
              50              55              60
Arg Glu Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys
65              70              75              80
Leu Tyr Gln Val Ile Ser Thr Pro Ser Asp Ile Phe Met Val Met Glu
              85              90              95
Tyr Val Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys Asn Gly Arg
              100             105             110
Leu Asp Glu Lys Glu Ser Arg Arg Leu Phe Gln Gln Ile Leu Ser Gly
              115             120             125
Val Asp Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro
              130             135             140
Glu Asn Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe
145             150             155             160
Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys
              165             170             175
Gly Ser Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr
              180             185             190
Ala Gly Pro Glu Val Asp Ile Trp Ser Ser Gly Val Ile Leu Tyr Ala
              195             200             205
Leu Leu Cys Gly Thr Leu Pro Phe Asp Asp Asp His Val Pro Thr Leu
              210             215             220
Phe Lys Lys Ile Cys Asp Gly Ile Phe Tyr Thr Pro Gln Tyr Leu Asn
225             230             235             240
Pro Ser Val Ile Ser Leu Leu Lys His Met Leu Gln Val Asp Pro Met
              245             250             255
Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln
              260             265             270
Asp Leu Pro Lys Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Ser Ser Thr
              275             280             285
  
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Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys	290	295	300
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp	305	310	315
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met	320	325	330
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe	340	345	350
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe	355	360	365
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn	370	375	380
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu	385	390	395
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys	400	405	410
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr	415	420	425
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys	430	435	440
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp	445	450	455
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala	460	465	470
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg	475	480	485
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu	490	495	500
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro	505	510	515
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu	520	525	530
Ile	Lys	Ile	Leu	Ala	Gln											535	540	545

<210> SEQ ID NO 2

<211> LENGTH: 550

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 2

Met	Ala	Thr	Ala	Glu	Lys	Gln	Lys	His	Asp	Gly	Arg	Val	Lys	Ile	Gly	1	5	10	15
His	Tyr	Ile	Leu	Gly	Asp	Thr	Leu	Gly	Val	Gly	Thr	Phe	Gly	Lys	Val	20	25	30	
Lys	Val	Gly	Lys	His	Glu	Leu	Thr	Gly	His	Lys	Val	Ala	Val	Lys	Ile	35	40	45	
Leu	Asn	Arg	Gln	Lys	Ile	Arg	Ser	Leu	Asp	Val	Val	Gly	Lys	Ile	Arg	50	55	60	
Arg	Glu	Ile	Gln	Asn	Leu	Lys	Leu	Phe	Arg	His	Pro	His	Ile	Ile	Lys	65	70	75	80
Leu	Tyr	Gln	Val	Ile	Ser	Thr	Pro	Ser	Asp	Ile	Phe	Met	Val	Met	Glu	85	90	95	
Tyr	Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Tyr	Ile	Cys	Lys	Asn	Gly	Arg	100	105	110	
Leu	Asp	Glu	Lys	Glu	Ser	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Gly	115	120	125	
Val	Asp	Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro	130	135	140	

Glu	Asn	Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe
145					150					155					160
Gly	Leu	Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys
			165						170					175	
Gly	Ser	Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr
			180					185					190		
Ala	Gly	Pro	Glu	Val	Asp	Ile	Trp	Ser	Ser	Gly	Val	Ile	Leu	Tyr	Ala
		195					200					205			
Leu	Leu	Cys	Gly	Thr	Leu	Pro	Phe	Asp	Asp	Asp	His	Val	Pro	Thr	Leu
	210					215					220				
Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn
225				230						235					240
Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met
			245						250					255	
Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln
			260					265					270		
Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr
		275					280					285			
Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys
	290					295				300					
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp
305					310					315					320
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met
			325						330					335	
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe
			340					345					350		
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe
	355						360					365			
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn
	370					375					380				
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu
385				390						395					400
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys
			405						410				415		
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr
		420						425					430		
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys
	435						440					445			
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp
	450					455					460				
Phe	Arg	Ser	Ile	Asp	Asp	Glu	Ile	Thr	Glu	Ala	Lys	Ser	Gly	Thr	Ala
465				470						475					480
Thr	Pro	Gln	Arg	Ser	Gly	Ser	Val	Ser	Asn	Tyr	Arg	Ser	Cys	Gln	Arg
			485						490				495		
Ser	Asp	Ser	Asp	Ala	Glu	Ala	Gln	Gly	Lys	Ser	Ser	Glu	Val	Ser	Leu
			500					505					510		
Thr	Ser	Ser	Val	Thr	Ser	Leu	Asp	Ser	Ser	Pro	Val	Asp	Leu	Thr	Pro
	515						520					525			
Arg	Pro	Gly	Ser	His	Thr	Ile	Glu	Phe	Phe	Glu	Met	Cys	Ala	Asn	Leu
	530					535					540				
Ile	Lys	Ile	Leu	Ala	Gln										
545					550										

210> SEQ ID NO 3

<211> LENGTH: 550

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 3

Met	Ala	Thr	Ala	Glu	Lys	Gln	Lys	His	Asp	Gly	Arg	Val	Lys	Ile	Gly
1				5					10					15	
His	Tyr	Ile	Leu	Gly	Asp	Thr	Leu	Gly	Val	Gly	Thr	Phe	Gly	Lys	Val
			20					25					30		
Lys	Val	Gly	Lys	His	Glu	Leu	Thr	Gly	His	Lys	Val	Ala	Val	Lys	Ile
		35					40					45			
Leu	Asn	Arg	Gln	Lys	Ile	Arg	Ser	Leu	Asp	Val	Val	Gly	Lys	Ile	Arg
	50					55					60				
Arg	Glu	Ile	Gln	Asn	Leu	Lys	Leu	Phe	Arg	His	Pro	His	Ile	Ile	Lys
65					70					75				80	
Leu	Tyr	Gln	Val	Ile	Ser	Thr	Pro	Ser	Asp	Ile	Phe	Met	Val	Met	Glu
				85					90					95	
Tyr	Val	Ser	Gly	Gly	Glu	Leu	Phe	Asp	Tyr	Ile	Cys	Lys	Asn	Gly	Arg
			100					105					110		
Leu	Asp	Glu	Lys	Glu	Ser	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Gly
		115					120					125			
Val	Asp	Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro
	130					135					140				
Glu	Asn	Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe
145					150					155				160	
Gly	Leu	Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys
			165					170						175	
Gly	Ser	Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr
			180					185					190		
Ala	Gly	Pro	Glu	Val	Asp	Ile	Trp	Ser	Ser	Gly	Val	Ile	Leu	Tyr	Ala
		195					200					205			
Leu	Leu	Cys	Gly	Thr	Leu	Pro	Phe	Asp	Asp	Asp	His	Val	Pro	Thr	Leu
	210					215					220				
Phe	Lys	Lys	Ile	Cys	Asp	Gly	Ile	Phe	Tyr	Thr	Pro	Gln	Tyr	Leu	Asn
225					230					235				240	
Pro	Ser	Val	Ile	Ser	Leu	Leu	Lys	His	Met	Leu	Gln	Val	Asp	Pro	Met
				245					250					255	
Lys	Arg	Ala	Ser	Ile	Lys	Asp	Ile	Arg	Glu	His	Glu	Trp	Phe	Lys	Gln
			260					265					270		
Asp	Leu	Pro	Lys	Tyr	Leu	Phe	Pro	Glu	Asp	Pro	Ser	Tyr	Ser	Ser	Thr
		275					280					285			
Met	Ile	Asp	Asp	Glu	Ala	Leu	Lys	Glu	Val	Cys	Glu	Lys	Phe	Glu	Cys
	290					295				300					
Ser	Glu	Glu	Glu	Val	Leu	Ser	Cys	Leu	Tyr	Asn	Arg	Asn	His	Gln	Asp
305					310					315				320	
Pro	Leu	Ala	Val	Ala	Tyr	His	Leu	Ile	Ile	Asp	Asn	Arg	Arg	Ile	Met
			325						330					335	
Asn	Glu	Ala	Lys	Asp	Phe	Tyr	Leu	Ala	Thr	Ser	Pro	Pro	Asp	Ser	Phe
		340						345					350		
Leu	Asp	Asp	His	His	Leu	Thr	Arg	Pro	His	Pro	Glu	Arg	Val	Pro	Phe
	355						360					365			
Leu	Val	Ala	Glu	Thr	Pro	Arg	Ala	Arg	His	Thr	Leu	Asp	Glu	Leu	Asn
	370					375					380				
Pro	Gln	Lys	Ser	Lys	His	Gln	Gly	Val	Arg	Lys	Ala	Lys	Trp	His	Leu
385					390					395				400	
Gly	Ile	Arg	Ser	Gln	Ser	Arg	Pro	Asn	Asp	Ile	Met	Ala	Glu	Val	Cys
			405						410					415	
Arg	Ala	Ile	Lys	Gln	Leu	Asp	Tyr	Glu	Trp	Lys	Val	Val	Asn	Pro	Tyr
			420					425					430		
Tyr	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Ser	Thr	Tyr	Ser	Lys
		435					440					445			
Met	Ser	Leu	Gln	Leu	Tyr	Gln	Val	Asp	Ser	Arg	Thr	Tyr	Leu	Leu	Asp

450		455		460
Phe Arg Ser Ile Asp Asp Glu Ile Thr Glu Ala Lys Ser Gly Thr Ala				
465		470		475
Thr Pro Gln Arg Ser Gly Ser Val Ser Asn Tyr Arg Ser Cys Gln Arg				480
	485		490	
Ser Asp Ser Asp Ala Glu Ala Gln Gly Lys Ser Ser Glu Val Ser Leu				495
	500		505	
Thr Ser Ser Val Thr Ser Leu Asp Ser Ser Pro Val Asp Leu Thr Pro				510
	515		520	
Arg Pro Gly Ser His Thr Ile Glu Phe Phe Glu Met Cys Ala Asn Leu				525
	530		535	
Ile Lys Ile Leu Ala Gln				540
545		550		

<210> SEQ ID NO 4

<211> LENGTH: 520

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 4

Gly Glu His Gln Leu Thr Gly His Lys Val Ala Val Lys Ile Leu Asn				
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Arg Gln Lys Ile Arg Ser Leu Asp Val Val Gly Lys Ile Lys Arg Glu				
	20	25	30	
Ile Gln Asn Leu Lys Leu Phe Arg His Pro His Ile Ile Lys Leu Tyr				
	35	40	45	
Gln Val Ile Ser Thr Pro Thr Asp Phe Phe Met Val Met Glu Tyr Val				
	50	55	60	
Ser Gly Gly Glu Leu Phe Asp Tyr Ile Cys Lys His Gly Arg Val Glu				
65	70	75	80	
Glu Met Glu Ala Arg Arg Leu Phe Gln Gln Ile Leu Ser Ala Val Asp				
	85	90	95	
Tyr Cys His Arg His Met Val Val His Arg Asp Leu Lys Pro Glu Asn				
	100	105	110	
Val Leu Leu Asp Ala His Met Asn Ala Lys Ile Ala Asp Phe Gly Leu				
	115	120	125	
Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly Ser				
	130	135	140	
Pro Asn Tyr Ala Ala Pro Glu Val Ile Ser Gly Arg Leu Tyr Ala Gly				
145	150	155	160	
Pro Glu Val Asp Ile Trp Ser Cys Gly Val Ile Leu Tyr Ala Leu Leu				
	165	170	175	
Cys Gly Thr Leu Pro Phe Asp Asp Glu His Val Pro Thr Leu Phe Lys				
	180	185	190	
Lys Ile Arg Gly Gly Val Phe Tyr Ile Pro Glu Tyr Leu Asn Arg Ser				
	195	200	205	
Val Ala Thr Leu Leu Met His Met Leu Gln Val Asp Pro Leu Lys Arg				
	210	215	220	
Ala Thr Ile Lys Asp Ile Arg Glu His Glu Trp Phe Lys Gln Asp Leu				
225	230	235	240	
Pro Ser Tyr Leu Phe Pro Glu Asp Pro Ser Tyr Asp Ala Asn Val Ile				
	245	250	255	
Asp Asp Glu Ala Val Lys Glu Val Cys Glu Lys Phe Glu Cys Thr Glu				
	260	265	270	
Ser Glu Val Met Asn Ser Leu Tyr Ser Gly Asp Pro Gln Asp Gln Leu				
	275	280	285	
Ala Val Ala Tyr His Leu Ile Ile Asp Asn Arg Arg Ile Met Asn Gln				
	290	295	300	
Ala Ser Glu Phe Tyr Leu Ala Ser Ser Pro Pro Ser Gly Ser Phe Met				

305		310		315		320									
Asp	Asp	Ser	Ala	Met	His	Ile	Pro	Pro	Gly	Leu	Lys	Pro	His	Pro	Glu
				325					330					335	
Arg	Met	Pro	Pro	Leu	Ile	Ala	Asp	Ser	Pro	Lys	Ala	Arg	Cys	Pro	Leu
				340					345					350	
Asp	Ala	Leu	Asn	Thr	Thr	Lys	Pro	Lys	Ser	Leu	Ala	Val	Lys	Lys	Ala
				355					360					365	
Lys	Trp	His	Leu	Gly	Ile	Arg	Ser	Gln	Ser	Lys	Pro	Tyr	Asp	Ile	Met
				370					375					380	
Ala	Glu	Val	Tyr	Arg	Ala	Met	Lys	Gln	Leu	Asp	Phe	Glu	Trp	Lys	Val
385									390						400
Val	Asn	Ala	Tyr	His	Leu	Arg	Val	Arg	Arg	Lys	Asn	Pro	Val	Thr	Gly
				405					410					415	
Asn	Tyr	Val	Lys	Met	Ser	Leu	Gln	Leu	Tyr	Leu	Val	Asp	Asn	Arg	Ser
				420					425					430	
Tyr	Leu	Leu	Asp	Phe	Lys	Ser	Ile	Asp	Asp	Glu	Val	Val	Glu	Gln	Arg
				435					440					445	
Ser	Gly	Ser	Ser	Thr	Pro	Gln	Arg	Ser	Cys	Ser	Ala	Ala	Gly	Leu	His
				450					455					460	
Arg	Pro	Arg	Ser	Ser	Phe	Asp	Ser	Thr	Thr	Ala	Glu	Ser	His	Ser	Leu
465									470						480
Ser	Gly	Ser	Leu	Thr	Gly	Ser	Leu	Thr	Gly	Ser	Thr	Leu	Ser	Ser	Val
				485					490						495
Ser	Pro	Arg	Leu	Gly	Ser	His	Thr	Met	Asp	Phe	Phe	Glu	Met	Cys	Ala
				500					505					510	
Ser	Leu	Ile	Thr	Thr	Leu	Ala	Arg								
				515					520						

<210> SEQ ID NO 5

<211> LENGTH: 552

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 5

Met	Ala	Glu	Lys	Gln	Lys	His	Asp	Gly	Arg	Val	Lys	Ile	Gly	His	Tyr
1				5					10					15	
Val	Leu	Gly	Asp	Thr	Leu	Gly	Val	Gly	Thr	Phe	Gly	Lys	Val	Lys	Ile
				20					25					30	
Gly	Glu	His	Gln	Leu	Thr	Gly	His	Lys	Val	Ala	Val	Lys	Ile	Leu	Asn
				35					40					45	
Arg	Gln	Lys	Ile	Arg	Ser	Leu	Asp	Val	Val	Gly	Lys	Ile	Lys	Arg	Glu
				50					55					60	
Ile	Gln	Asn	Leu	Lys	Leu	Phe	Arg	His	Pro	His	Ile	Ile	Lys	Leu	Tyr
65									70					75	80
Gln	Val	Ile	Ser	Thr	Pro	Thr	Asp	Phe	Phe	Met	Val	Met	Glu	Tyr	Val
				85					90					95	
Ser	Gly	Gly	Glu	Leu	Phe	Asp	Tyr	Ile	Cys	Lys	His	Gly	Arg	Val	Glu
				100					105					110	
Glu	Met	Glu	Ala	Arg	Arg	Leu	Phe	Gln	Gln	Ile	Leu	Ser	Ala	Val	Asp
				115					120					125	
Tyr	Cys	His	Arg	His	Met	Val	Val	His	Arg	Asp	Leu	Lys	Pro	Glu	Asn
				130					135					140	
Val	Leu	Leu	Asp	Ala	His	Met	Asn	Ala	Lys	Ile	Ala	Asp	Phe	Gly	Leu
145									150					155	160
Ser	Asn	Met	Met	Ser	Asp	Gly	Glu	Phe	Leu	Arg	Thr	Ser	Cys	Gly	Ser
				165					170					175	
Pro	Asn	Tyr	Ala	Ala	Pro	Glu	Val	Ile	Ser	Gly	Arg	Leu	Tyr	Ala	Gly
				180					185					190	
Pro	Glu	Val	Asp	Ile	Trp	Ser	Cys	Gly	Val	Ile	Leu	Tyr	Ala	Leu	Leu

50		55		60
Glu Val Leu Asp Ser	Glu Thr Leu Cys Arg	Arg Ala Val Lys Ile Leu		
65	70	75	80	
Lys Lys Lys Lys Leu	Arg Arg Ile Pro Asn	Gly Glu Ala Asn Val Lys		
	85	90	95	
Lys Glu Ile Gln Leu	Leu Arg Arg Leu Arg	His Lys Asn Val Ile Gln		
	100	105	110	
Leu Val Asp Val Leu	Tyr Asn Glu Glu Lys	Gln Lys Met Tyr Met Val		
	115	120	125	
Met Glu Tyr Cys Val	Cys Gly Met Gln Glu	Met Leu Asp Ser Val Pro		
	130	135	140	
Glu Lys Arg Phe Pro	Val Cys Gln Ala His	Gly Tyr Phe Cys Gln Leu		
145	150	155	160	
Ile Asp Gly Leu Glu	Tyr Leu His Ser Gln	Gly Ile Val His Lys Asp		
	165	170	175	
Ile Lys Pro Gly Asn	Leu Leu Leu Thr Thr	Gly Gly Thr Leu Lys Ile		
	180	185	190	
Ser Asp Leu Gly Val	Ala Glu Ala Leu His	Pro Phe Ala Ala Asp Asp		
	195	200	205	
Thr Cys Arg Thr Ser	Gln Gly Ser Pro Ala	Phe Gln Pro Pro Glu Ile		
	210	215	220	
Ala Asn Gly Leu Asp	Thr Phe Ser Gly Phe	Lys Val Asp Ile Trp Ser		
225	230	235	240	
Ala Gly Val Thr Leu	Tyr Asn Ile Thr Thr	Gly Leu Tyr Pro Phe Glu		
	245	250	255	
Gly Asp Asn Ile Tyr	Lys Leu Phe Glu Asn	Ile Gly Lys Gly Ser Tyr		
	260	265	270	
Ala Ile Pro Gly Asp	Cys Gly Pro Pro Leu	Ser Asp Leu Leu Lys Gly		
	275	280	285	
Met Leu Glu Tyr Glu	Pro Ala Lys Arg Phe	Ser Ile Arg Gln Ile Arg		
	290	295	300	
Gln His Ser Trp Phe	Arg Lys Lys His Pro	Pro Ala Glu Ala Pro Val		
305	310	315	320	
Pro Ile Pro Pro Ser	Pro Asp Thr Lys Asp	Arg Trp Arg Ser Met Thr		
	325	330	335	
Val Val Pro Tyr Leu	Glu Asp Leu His Gly	Ala Asp Glu Asp Glu Asp		
	340	345	350	
Leu Phe Asp Ile Glu	Asp Asp Ile Ile Tyr	Thr Gln Asp Phe Thr Val		
	355	360	365	
Pro Gly Gln Val Pro	Glu Glu Glu Ala Ser	His Asn Gly Gln Arg Arg		
	370	375	380	
Gly Leu Pro Lys Ala	Val Cys Met Asn Gly	Thr Glu Ala Ala Gln Leu		
385	390	395	400	
Ser Thr Lys Ser Arg	Ala Glu Gly Arg Ala	Pro Asn Pro Ala Arg Lys		
	405	410	415	
Ala Cys Ser Ala Ser	Ser Lys Ile Arg Arg	Leu Ser Ala Cys Lys Gln		
	420	425	430	

Gln

<210> SEQ ID NO 7

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 7

Met Glu Val Val Asp	Pro Gln Gln Leu Gly	Met Phe Thr Glu Gly Glu
1	5	10
Leu Met Ser Val Gly	Met Asp Thr Phe Ile	His Arg Ile Asp Ser Thr
	20	25
		30

Glu	Val	Ile	Tyr	Gln	Pro	Arg	Arg	Lys	Arg	Ala	Lys	Leu	Ile	Gly	Lys	35	40	45
Tyr	Leu	Met	Gly	Asp	Leu	Leu	Gly	Glu	Gly	Ser	Tyr	Gly	Lys	Val	Lys	50	55	60
Glu	Val	Leu	Asp	Ser	Glu	Thr	Leu	Cys	Arg	Arg	Ala	Val	Lys	Ile	Leu	65	70	75
Lys	Lys	Lys	Lys	Leu	Arg	Arg	Ile	Pro	Asn	Gly	Glu	Ala	Asn	Val	Lys	85	90	95
Lys	Glu	Ile	Gln	Leu	Leu	Arg	Arg	Leu	Arg	His	Lys	Asn	Val	Ile	Gln	100	105	110
Leu	Val	Asp	Val	Leu	Tyr	Asn	Glu	Lys	Gln	Lys	Met	Tyr	Met	Val		115	120	125
Met	Glu	Tyr	Cys	Val	Cys	Gly	Met	Gln	Glu	Met	Leu	Asp	Ser	Val	Pro	130	135	140
Glu	Lys	Arg	Phe	Pro	Val	Cys	Gln	Ala	His	Gly	Tyr	Phe	Cys	Gln	Leu	145	150	155
Ile	Asp	Gly	Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Ile	Val	His	Lys	Asp	165	170	175
Ile	Lys	Pro	Gly	Asn	Leu	Leu	Leu	Thr	Thr	Gly	Gly	Thr	Leu	Lys	Ile	180	185	190
Ser	Asp	Leu	Gly	Val	Ala	Glu	Ala	Leu	His	Pro	Phe	Ala	Ala	Asp	Asp	195	200	205
Thr	Cys	Arg	Thr	Ser	Gln	Gly	Ser	Pro	Ala	Phe	Gln	Pro	Pro	Glu	Ile	210	215	220
Ala	Asn	Gly	Leu	Asp	Thr	Phe	Ser	Gly	Phe	Lys	Val	Asp	Ile	Trp	Ser	225	230	235
Ala	Gly	Val	Thr	Leu	Tyr	Asn	Ile	Thr	Thr	Gly	Leu	Tyr	Pro	Phe	Glu	245	250	255
Gly	Asp	Asn	Ile	Tyr	Lys	Leu	Phe	Glu	Asn	Ile	Gly	Lys	Gly	Ser	Tyr	260	265	270
Ala	Ile	Pro	Gly	Asp	Cys	Gly	Pro	Pro	Leu	Ser	Asp	Leu	Leu	Lys	Gly	275	280	285
Met	Leu	Glu	Tyr	Glu	Pro	Ala	Lys	Arg	Phe	Ser	Ile	Arg	Gln	Ile	Arg	290	295	300
Gln	His	Ser	Trp	Phe	Arg	Lys	Lys	His	Pro	Pro	Ala	Glu	Ala	Pro	Val	305	310	315
Pro	Ile	Pro	Pro	Ser	Pro	Asp	Thr	Lys	Asp	Arg	Trp	Arg	Ser	Met	Thr	325	330	335
Val	Val	Pro	Tyr	Leu	Glu	Asp	Leu	His	Gly	Ala	Asp	Glu	Asp	Glu	Asp	340	345	350
Leu	Phe	Asp	Ile	Glu	Asp	Asp	Ile	Ile	Tyr	Thr	Gln	Asp	Phe	Thr	Val	355	360	365
Pro	Gly	Gln	Val	Pro	Glu	Glu	Glu	Ala	Ser	His	Asn	Gly	Gln	Arg	Arg	370	375	380
Gly	Leu	Pro	Lys	Ala	Val	Cys	Met	Asn	Gly	Thr	Glu	Ala	Ala	Gln	Leu	385	390	395
Ser	Thr	Lys	Ser	Arg	Ala	Glu	Gly	Arg	Ala	Pro	Asn	Pro	Ala	Arg	Lys	405	410	415
Ala	Cys	Ser	Ala	Ser	Ser	Lys	Ile	Arg	Arg	Leu	Ser	Ala	Cys	Lys	Gln	420	425	430

Gln

<210> SEQ ID NO 8

<211> LENGTH: 433

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 8

Met Glu Val Val Asp Pro Gln Gln Leu Gly Met Phe Thr Glu Gly Glu

1				5					10				15			
Leu	Met	Ser	Val	Gly	Met	Asp	Thr	Phe	Ile	His	Arg	Ile	Asp	Ser	Thr	
			20					25					30			
Glu	Val	Ile	Tyr	Gln	Pro	Arg	Arg	Lys	Arg	Ala	Lys	Leu	Ile	Gly	Lys	
		35					40					45				
Tyr	Leu	Met	Gly	Asp	Leu	Leu	Gly	Glu	Gly	Ser	Tyr	Gly	Lys	Val	Lys	
	50					55					60					
Glu	Val	Leu	Asp	Ser	Glu	Thr	Leu	Cys	Arg	Arg	Ala	Val	Lys	Ile	Leu	
65					70				75						80	
Lys	Lys	Lys	Lys	Leu	Arg	Arg	Ile	Pro	Asn	Gly	Glu	Ala	Asn	Val	Lys	
				85					90					95		
Lys	Glu	Ile	Gln	Leu	Leu	Arg	Arg	Leu	Arg	His	Lys	Asn	Val	Ile	Gln	
			100					105					110			
Leu	Val	Asp	Val	Leu	Tyr	Asn	Glu	Glu	Lys	Gln	Lys	Met	Tyr	Met	Val	
		115					120					125				
Met	Glu	Tyr	Cys	Val	Cys	Gly	Met	Gln	Glu	Met	Leu	Asp	Ser	Val	Pro	
	130					135					140					
Glu	Lys	Arg	Phe	Pro	Val	Cys	Gln	Ala	His	Gly	Tyr	Phe	Cys	Gln	Leu	
145					150					155					160	
Ile	Asp	Gly	Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Ile	Val	His	Lys	Asp	
			165						170					175		
Ile	Lys	Pro	Gly	Asn	Leu	Leu	Leu	Thr	Thr	Gly	Gly	Thr	Leu	Lys	Ile	
			180					185					190			
Ser	Asp	Leu	Gly	Val	Ala	Glu	Ala	Leu	His	Pro	Phe	Ala	Ala	Asp	Asp	
	195						200					205				
Thr	Cys	Arg	Thr	Ser	Gln	Gly	Ser	Pro	Ala	Phe	Gln	Pro	Pro	Glu	Ile	
	210					215					220					
Ala	Asn	Gly	Leu	Asp	Thr	Phe	Ser	Gly	Phe	Lys	Val	Asp	Ile	Trp	Ser	
225					230					235					240	
Ala	Gly	Val	Thr	Leu	Tyr	Asn	Ile	Thr	Thr	Gly	Leu	Tyr	Pro	Phe	Glu	
			245						250					255		
Gly	Asp	Asn	Ile	Tyr	Lys	Leu	Phe	Glu	Asn	Ile	Gly	Lys	Gly	Ser	Tyr	
		260						265					270			
Ala	Ile	Pro	Gly	Asp	Cys	Gly	Pro	Pro	Leu	Ser	Asp	Leu	Leu	Lys	Gly	
		275					280					285				
Met	Leu	Glu	Tyr	Glu	Pro	Ala	Lys	Arg	Phe	Ser	Ile	Arg	Gln	Ile	Arg	
	290					295					300					
Gln	His	Ser	Trp	Phe	Arg	Lys	Lys	His	Pro	Pro	Ala	Glu	Ala	Pro	Val	
305					310					315					320	
Pro	Ile	Pro	Pro	Ser	Pro	Asp	Thr	Lys	Asp	Arg	Trp	Arg	Ser	Met	Thr	
			325						330					335		
Val	Val	Pro	Tyr	Leu	Glu	Asp	Leu	His	Gly	Ala	Asp	Glu	Asp	Glu	Asp	
		340						345					350			
Leu	Phe	Asp	Ile	Glu	Asp	Asp	Ile	Ile	Tyr	Thr	Gln	Asp	Phe	Thr	Val	
	355						360					365				
Pro	Gly	Gln	Val	Pro	Glu	Glu	Ala	Ser	His	Asn	Gly	Gln	Arg	Arg		
	370					375				380						
Gly	Leu	Pro	Lys	Ala	Val	Cys	Met	Asn	Gly	Thr	Glu	Ala	Ala	Gln	Leu	
385					390					395					400	
Ser	Thr	Lys	Ser	Arg	Ala	Glu	Gly	Arg	Ala	Pro	Asn	Pro	Ala	Arg	Lys	
			405						410					415		
Ala	Cys	Ser	Ala	Ser	Ser	Lys	Ile	Arg	Arg	Leu	Ser	Ala	Cys	Lys	Gln	
			420					425					430			

Gln

<210> SEQ ID NO 9

<211> LENGTH: 431

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 9

```
Met Ser Phe Leu Val Ser Lys Pro Glu Arg Ile Arg Arg Trp Val Ser
1          5          10          15
Glu Lys Phe Ile Val Glu Gly Leu Arg Asp Leu Glu Leu Phe Gly Glu
20          25          30
Gln Pro Pro Gly Asp Thr Arg Arg Lys Thr Asn Asp Ala Ser Ser Glu
35          40          45
Ser Ile Ala Ser Phe Ser Lys Gln Glu Val Met Ser Ser Phe Leu Pro
50          55          60
Glu Gly Gly Cys Tyr Glu Leu Leu Thr Val Ile Gly Lys Gly Phe Glu
65          70          75          80
Asp Leu Met Thr Val Asn Leu Ala Arg Tyr Lys Pro Thr Gly Glu Tyr
85          90          95
Val Thr Val Arg Arg Ile Asn Leu Glu Ala Cys Ser Asn Glu Met Val
100          105          110
Thr Phe Leu Gln Gly Glu Leu His Val Ser Lys Leu Phe Asn His Pro
115          120          125
Asn Ile Val Pro Tyr Arg Ala Thr Phe Ile Ala Asp Asn Glu Leu Trp
130          135          140
Val Val Thr Ser Phe Met Ala Tyr Gly Ser Ala Lys Asp Leu Ile Cys
145          150          155          160
Thr His Phe Met Asp Gly Met Asn Glu Leu Ala Ile Ala Tyr Ile Leu
165          170          175
Gln Gly Val Leu Lys Ala Leu Asp Tyr Ile His His Met Gly Tyr Val
180          185          190
His Arg Ser Val Lys Ala Ser His Ile Leu Ile Ser Val Asp Gly Lys
195          200          205
Val Tyr Leu Ser Gly Leu Arg Ser Asn Leu Ser Met Ile Ser His Gly
210          215          220
Gln Arg Gln Arg Val Val His Asp Phe Pro Lys Tyr Ser Val Lys Val
225          230          235          240
Leu Pro Trp Leu Ser Pro Glu Val Leu Gln Gln Asn Leu Gln Gly Tyr
245          250          255
Asp Ala Lys Ser Asp Ile Tyr Ser Val Gly Ile Thr Ala Cys Glu Leu
260          265          270
Ala Asn Gly His Val Pro Phe Lys Asp Met Pro Ala Thr Gln Met Leu
275          280          285
Leu Glu Lys Leu Asn Gly Thr Val Pro Cys Leu Leu Asp Thr Ser Thr
290          295          300
Ile Pro Ala Glu Glu Leu Thr Met Ser Pro Ser Arg Ser Val Ala Asn
305          310          315          320
Ser Gly Leu Ser Asp Ser Leu Thr Thr Ser Thr Pro Arg Pro Ser Asn
325          330          335
Gly Asp Trp Pro Ser His Pro Tyr His Arg Thr Phe Ser Pro His Phe
340          345          350
His His Phe Val Glu Gln Cys Leu Gln Arg Asn Pro Asp Ala Arg Pro
355          360          365
Ser Ala Ser Thr Leu Leu Asn His Ser Phe Phe Lys Gln Ile Lys Arg
370          375          380
Arg Ala Ser Lys Ala Leu Pro Glu Leu Leu Arg Pro Val Thr Pro Ile
385          390          395          400
Thr Asn Phe Glu Gly Ser Gln Ser Gln Asp His Ser Gly Ile Phe Gly
405          410          415
Leu Val Thr Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Phe
420          425          430
```

<210> SEQ ID NO 10

<211> LENGTH: 418

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 10

```
Met Ser Leu Leu Asp Cys Phe Cys Thr Ser Arg Thr Gln Val Glu Ser
1      5      10      15
Leu Arg Pro Glu Lys Gln Ser Glu Thr Ser Ile His Gln Tyr Leu Val
20      25      30
Asp Glu Pro Thr Leu Ser Trp Ser Arg Pro Ser Thr Arg Ala Ser Glu
35      40      45
Val Leu Cys Ser Thr Asn Val Ser His Tyr Glu Leu Gln Val Glu Ile
50      55      60
Gly Arg Gly Phe Asp Asn Leu Thr Ser Val His Leu Ala Arg His Thr
65      70      75      80
Pro Thr Gly Thr Leu Val Thr Ile Lys Ile Thr Asn Leu Glu Asn Cys
85      90      95
Asn Glu Glu Arg Leu Lys Ala Leu Gln Lys Ala Val Ile Leu Ser His
100     105     110
Phe Phe Arg His Pro Asn Ile Thr Thr Tyr Trp Thr Val Phe Thr Val
115     120     125
Gly Ser Trp Leu Trp Val Ile Ser Pro Phe Met Ala Tyr Gly Ser Ala
130     135     140
Ser Gln Leu Leu Arg Thr Tyr Phe Pro Glu Gly Met Ser Glu Thr Leu
145     150     155     160
Ile Arg Asn Ile Leu Phe Gly Ala Val Arg Gly Leu Asn Tyr Leu His
165     170     175
Gln Asn Gly Cys Ile His Arg Ser Ile Lys Ala Ser His Ile Leu Ile
180     185     190
Ser Gly Asp Gly Leu Val Thr Leu Ser Gly Leu Ser His Leu His Ser
195     200     205
Leu Val Lys His Gly Gln Arg His Arg Ala Val Tyr Asp Phe Pro Gln
210     215     220
Phe Ser Thr Ser Val Gln Pro Trp Leu Ser Pro Glu Leu Leu Arg Gln
225     230     235     240
Asp Leu His Gly Tyr Asn Val Lys Ser Asp Ile Tyr Ser Val Gly Ile
245     250     255
Thr Ala Cys Glu Leu Ala Ser Gly Gln Val Pro Phe Gln Asp Met His
260     265     270
Arg Thr Gln Met Leu Leu Gln Lys Leu Lys Gly Pro Pro Tyr Ser Pro
275     280     285
Leu Asp Ile Ser Ile Phe Pro Gln Ser Glu Ser Arg Met Lys Asn Ser
290     295     300
Gln Ser Gly Val Asp Ser Gly Ile Gly Glu Ser Val Leu Val Ser Ser
305     310     315     320
Gly Thr His Thr Val Asn Ser Asp Arg Leu His Thr Pro Ser Ser Lys
325     330     335
Thr Phe Ser Pro Ala Phe Phe Ser Leu Val Gln Leu Cys Leu Gln Gln
340     345     350
Asp Pro Glu Lys Arg Pro Ser Ala Ser Ser Leu Leu Ser His Val Phe
355     360     365
Phe Lys Gln Met Lys Glu Glu Ser Gln Asp Ser Ile Leu Ser Leu Leu
370     375     380
Pro Pro Ala Tyr Asn Lys Pro Ser Ile Ser Leu Pro Pro Val Leu Pro
385     390     395     400
Trp Thr Glu Pro Glu Cys Asp Phe Pro Asp Glu Lys Asp Ser Tyr Trp
405     410     415
Glu Phe
```

210> SEQ ID NO 11

<211> LENGTH: 341

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 11

```
Met Pro Phe Pro Phe Gly Lys Ser His Lys Ser Pro Ala Asp Ile Val
1          5          10          15
Lys Asn Leu Lys Glu Ser Met Ala Val Leu Glu Lys Gln Asp Ile Ser
          20          25          30
Asp Lys Lys Ala Glu Lys Ala Thr Glu Glu Val Ser Lys Asn Leu Val
          35          40          45
Ala Met Lys Glu Ile Leu Tyr Gly Thr Asn Glu Lys Glu Pro Gln Thr
          50          55          60
Glu Ala Val Ala Gln Leu Ala Gln Glu Leu Tyr Asn Ser Gly Leu Leu
65          70          75          80
Ser Thr Leu Val Ala Asp Leu Gln Leu Ile Asp Phe Glu Gly Lys Lys
          85          90          95
Asp Val Ala Gln Ile Phe Asn Asn Ile Leu Arg Arg Gln Ile Gly Thr
          100          105          110
Arg Thr Pro Thr Val Glu Tyr Ile Cys Thr Gln Gln Asn Ile Leu Phe
          115          120          125
Met Leu Leu Lys Gly Tyr Glu Ser Pro Glu Ile Ala Leu Asn Cys Gly
          130          135          140
Ile Met Leu Arg Glu Cys Ile Arg His Glu Pro Leu Ala Lys Ile Ile
145          150          155          160
Leu Trp Ser Glu Gln Phe Tyr Asp Phe Phe Arg Tyr Val Glu Met Ser
          165          170          175
Thr Phe Asp Ile Ala Ser Asp Ala Phe Ala Thr Phe Lys Asp Leu Leu
          180          185          190
Thr Arg His Lys Leu Leu Ser Ala Glu Phe Leu Glu Gln His Tyr Asp
          195          200          205
Arg Phe Phe Ser Glu Tyr Glu Lys Leu Leu His Ser Glu Asn Tyr Val
          210          215          220
Thr Lys Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
225          230          235          240
His Asn Phe Thr Ile Met Thr Lys Tyr Ile Ser Lys Pro Glu Asn Leu
          245          250          255
Lys Leu Met Met Asn Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Phe
          260          265          270
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Thr
          275          280          285
Gln Pro Ile Leu Asp Ile Leu Leu Lys Asn Gln Ala Lys Leu Ile Glu
          290          295          300
Phe Leu Ser Lys Phe Gln Asn Asp Arg Thr Glu Asp Glu Gln Phe Asn
305          310          315          320
Asp Glu Lys Thr Tyr Leu Val Lys Gln Ile Arg Asp Leu Lys Arg Pro
          325          330          335
Ala Gln Gln Glu Ala
          340
```

<210> SEQ ID NO 12

<211> LENGTH: 337

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 12

```
Met Lys Lys Met Pro Leu Phe Ser Lys Ser His Lys Asn Pro Ala Glu
1          5          10          15
Ile Val Lys Ile Leu Lys Asp Asn Leu Ala Ile Leu Glu Lys Gln Asp
```


Cys	Lys	Lys	Asp	Val	Ala	Ser	Val	Phe	Asn	Asn	Leu	Leu	Arg	Arg	Gln
			100					105					110		
Ile	Gly	Thr	Arg	Ser	Pro	Thr	Val	Glu	Tyr	Leu	Ala	Ala	Arg	Pro	Glu
		115					120					125			
Ile	Leu	Ile	Thr	Leu	Leu	Leu	Gly	Tyr	Glu	Gln	Pro	Asp	Ile	Ala	Leu
	130					135					140				
Thr	Cys	Gly	Ser	Met	Leu	Arg	Glu	Ala	Val	Arg	His	Glu	His	Leu	Ala
145					150					155					160
Arg	Ile	Val	Leu	Tyr	Ser	Glu	Tyr	Phe	Gln	Arg	Phe	Phe	Val	Phe	Val
			165						170						175
Gln	Ser	Asp	Val	Phe	Asp	Ile	Ala	Thr	Asp	Ala	Phe	Ser	Thr	Phe	Lys
			180					185					190		
Asp	Leu	Met	Thr	Lys	His	Lys	Asn	Met	Cys	Ala	Glu	Tyr	Leu	Asp	Asn
		195					200					205			
Asn	Tyr	Asp	Arg	Phe	Phe	Gly	Gln	Tyr	Ser	Ala	Leu	Thr	Asn	Ser	Glu
	210					215					220				
Asn	Tyr	Val	Thr	Arg	Arg	Gln	Ser	Leu	Lys	Leu	Leu	Gly	Glu	Leu	Leu
225					230					235					240
Leu	Asp	Arg	His	Asn	Phe	Ser	Thr	Met	Asn	Lys	Tyr	Ile	Thr	Ser	Pro
			245						250					255	
Glu	Asn	Leu	Lys	Thr	Val	Met	Glu	Leu	Leu	Arg	Asp	Lys	Arg	Arg	Asn
			260					265					270		
Ile	Gln	Tyr	Glu	Ala	Phe	His	Val	Phe	Lys	Ile	Phe	Val	Ala	Asn	Pro
		275					280					285			
Asn	Lys	Pro	Arg	Pro	Ile	Thr	Asp	Ile	Leu	Thr	Arg	Asn	Arg	Asp	Lys
	290					295					300				
Leu	Val	Glu	Phe	Leu	Thr	Ala	Phe	His	Asn	Asp	Arg	Thr	Asn	Asp	Glu
305					310					315					320
Gln	Phe	Asn	Asp	Glu	Lys	Ala	Tyr	Leu	Ile	Lys	Gln	Ile	Gln	Glu	Leu
			325						330					335	

Arg Val

<210> SEQ ID NO 14

<211> LENGTH: 636

<212> TYPE: PRT

<213> ORGANISM: Caenorhabditis elegans

<400> SEQUENCE: 14

Met	Asp	Ser	Thr	Thr	Ser	Leu	Pro	Asn	Asn	Val	Leu	Leu	Lys	Lys	Ala
1				5					10					15	
Arg	Pro	Ser	Lys	Ile	Phe	Ala	Val	Thr	Ser	Ala	Asn	Ala	Leu	Asn	Val
		20						25					30		
Lys	Thr	Glu	Pro	Val	Ile	Phe	Val	Lys	Ser	Asp	Asp	Leu	Asn	Gln	Ala
		35					40					45			
Asn	Thr	Pro	Leu	Thr	Gly	Ser	Lys	Phe	Gly	Thr	His	Leu	Ala	Cys	Ile
	50					55					60				
Arg	Thr	Ser	Cys	Leu	His	Arg	Thr	Val	Asn	Ala	Ser	Asn	Tyr	Ser	Thr
65					70					75				80	
Met	Ser	Asp	Gly	Gly	Leu	Tyr	Thr	Ser	Asp	Glu	Pro	Cys	Ser	Ser	Ala
			85						90					95	
Gln	Ala	Glu	Phe	Arg	Leu	Ala	Ala	His	Trp	Glu	Ser	Thr	Phe	Thr	Arg
			100					105					110		
Thr	Arg	Glu	Ile	His	Cys	Asp	Thr	Gly	Tyr	Ser	Ser	Gln	Ser	Pro	Pro
		115					120					125			
Glu	Thr	Thr	Val	Phe	Ile	Gln	Lys	Ser	Arg	Phe	Pro	Val	Ala	Glu	Lys
	130					135					140				
Pro	Gly	Thr	Pro	Glu	Leu	Lys	Ser	Phe	Glu	Ser	Lys	Lys	Leu	Val	Gln
145					150					155					160
Lys	Lys	Ser	Gly	Asn	Ala	Ser	Thr	Pro	Thr	Arg	Lys	Leu	Ala	Ser	Glu

				165					170					175			
Glu	Lys	Lys	Ala	Lys	Asn	Thr	Ser	Met	Gly	Gln	Thr	Pro	Ser	Lys	Leu		
			180					185					190				
Lys	Ser	Pro	Lys	Ala	Leu	Lys	Met	Val	Lys	Lys	Glu	Asn	Glu	Pro	Ala		
		195					200					205					
Ile	Pro	Pro	Asn	His	Phe	Glu	Gly	Lys	Val	Tyr	Gly	Tyr	Leu	Val	Asp		
	210					215					220						
Asp	Met	Ser	Ala	Ile	Gly	Ile	Gln	Pro	Ile	Leu	Asp	Lys	Tyr	Asn	Glu		
	225				230					235					240		
Asp	Pro	Glu	Lys	Phe	Phe	Lys	Arg	Phe	Asp	Ser	Lys	Pro	Trp	Phe	Arg		
			245					250						255			
Arg	Lys	Val	Met	Pro	Leu	Leu	Phe	Gly	Lys	Ser	His	Lys	Ser	Pro	Ala		
			260					265					270				
Asp	Val	Val	Lys	Thr	Leu	Arg	Glu	Val	Leu	Thr	Ile	Leu	Asp	Lys	Leu		
		275					280					285					
Pro	Pro	Pro	Lys	Leu	Asp	Lys	Asp	Gly	Asn	Ile	Gln	Ser	Asp	Lys	Lys		
	290					295					300						
Tyr	Asp	Lys	Ala	Leu	Asp	Glu	Val	Ser	Lys	Asn	Val	Ala	Met	Ile	Lys		
	305				310					315					320		
Ser	Phe	Ile	Tyr	Gly	Asn	Asp	Ser	Ala	Glu	Pro	Ser	Ser	Glu	His	Val		
			325					330						335			
Val	Gln	Val	Ala	Gln	Leu	Ala	Gln	Glu	Val	Tyr	Asn	Ala	Asn	Ile	Leu		
			340					345					350				
Pro	Met	Leu	Ile	Lys	Met	Leu	Pro	Lys	Phe	Glu	Phe	Glu	Cys	Lys	Lys		
		355					360					365					
Asp	Val	Gly	Gln	Ile	Phe	Asn	Asn	Leu	Leu	Arg	Arg	Gln	Ile	Gly	Thr		
	370					375					380						
Arg	Ser	Pro	Thr	Val	Glu	Tyr	Leu	Gly	Ala	Arg	Pro	Glu	Ile	Leu	Ile		
	385				390					395					400		
Gln	Leu	Val	Gln	Gly	Tyr	Ser	Val	Pro	Asp	Ile	Ala	Leu	Thr	Cys	Gly		
			405					410						415			
Leu	Met	Leu	Arg	Glu	Ser	Ile	Arg	His	Asp	His	Leu	Ala	Lys	Ile	Ile		
			420					425					430				
Leu	Tyr	Ser	Asp	Val	Phe	Tyr	Thr	Phe	Phe	Leu	Tyr	Val	Gln	Ser	Glu		
		435					440					445					
Val	Phe	Asp	Ile	Ser	Ser	Asp	Ala	Phe	Ser	Thr	Phe	Lys	Glu	Leu	Thr		
	450					455					460						
Thr	Arg	His	Lys	Ala	Ile	Ile	Ala	Glu	Phe	Leu	Asp	Ser	Asn	Tyr	Asp		
	465				470					475					480		
Thr	Phe	Phe	Ala	Gln	Tyr	Gln	Asn	Leu	Leu	Asn	Ser	Lys	Asn	Tyr	Val		
			485					490						495			
Thr	Arg	Arg	Gln	Ser	Leu	Lys	Leu	Leu	Gly	Glu	Leu	Leu	Leu	Asp	Arg		
			500					505					510				
His	Asn	Phe	Asn	Thr	Met	Thr	Lys	Tyr	Ile	Ser	Asn	Pro	Asp	Asn	Leu		
		515					520					525					
Arg	Leu	Met	Met	Glu	Leu	Leu	Arg	Asp	Lys	Ser	Arg	Asn	Ile	Gln	Tyr		
	530					535					540						
Glu	Ala	Phe	His	Val	Phe	Lys	Val	Phe	Val	Ala	Asn	Pro	Asn	Lys	Pro		
	545				550				555						560		
Lys	Pro	Ile	Ser	Asp	Ile	Leu	Asn	Arg	Asn	Arg	Glu	Lys	Leu	Val	Glu		
			565					570						575			
Phe	Leu	Ser	Glu	Phe	His	Asn	Asp	Arg	Thr	Asp	Asp	Glu	Gln	Phe	Asn		
			580				585					590					
Asp	Glu	Lys	Ala	Tyr	Leu	Ile	Lys	Gln	Ile	Gln	Glu	Met	Lys	Ser	Ser		
		595				600					605						
Pro	Lys	Glu	Ala	Lys	Lys	Pro	Lys	Ser	Lys	Glu	Asp	Glu	Asn	Gln	Glu		
	610					615					620						


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    Pro Ala Gly Pro Ser Glu Gly Pro Ser Thr Ser Gln
    625                      630                      635
<210> SEQ ID NO 15
<211> LENGTH: 339
<212> TYPE: PRT
<213> ORGANISM: Drosophila melanogaster
<400> SEQUENCE: 15
Met Pro Leu Phe Gly Lys Ser Gln Lys Ser Pro Val Glu Leu Val Lys
1                      5                      10                      15
Ser Leu Lys Glu Ala Ile Asn Ala Leu Glu Ala Gly Asp Arg Lys Val
20                      25                      30
Glu Lys Ala Gln Glu Asp Val Ser Lys Asn Leu Val Ser Ile Lys Asn
35                      40                      45
Met Leu Tyr Gly Ser Ser Asp Ala Glu Pro Pro Ala Asp Tyr Val Val
50                      55                      60
Ala Gln Leu Ser Gln Glu Leu Tyr Asn Ser Asn Leu Leu Leu Leu Leu
65                      70                      75                      80
Ile Gln Asn Leu His Arg Ile Asp Phe Glu Gly Lys Lys His Val Ala
85                      90                      95
Leu Ile Phe Asn Asn Val Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
100                     105                     110
Thr Val Glu Tyr Ile Cys Thr Lys Pro Glu Ile Leu Phe Thr Leu Met
115                     120                     125
Ala Gly Tyr Glu Asp Ala His Pro Glu Ile Ala Leu Asn Ser Gly Thr
130                     135                     140
Met Leu Arg Glu Cys Ala Arg Tyr Glu Ala Leu Ala Lys Ile Met Leu
145                     150                     155                     160
His Ser Asp Glu Phe Phe Lys Phe Phe Arg Tyr Val Glu Val Ser Thr
165                     170                     175
Phe Asp Ile Ala Ser Asp Ala Phe Ser Thr Phe Lys Glu Leu Leu Thr
180                     185                     190
Arg His Lys Leu Leu Cys Ala Glu Phe Leu Asp Ala Asn Tyr Asp Lys
195                     200                     205
Phe Phe Ser Gln His Tyr Gln Arg Leu Leu Asn Ser Glu Asn Tyr Val
210                     215                     220
Thr Arg Arg Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg
225                     230                     235                     240
His Asn Phe Thr Val Met Thr Arg Tyr Ile Ser Glu Pro Glu Asn Leu
245                     250                     255
Lys Leu Met Met Asn Met Leu Lys Glu Lys Ser Arg Asn Ile Gln Phe
260                     265                     270
Glu Ala Phe His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Pro
275                     280                     285
Lys Pro Ile Leu Asp Ile Leu Leu Arg Asn Gln Thr Lys Leu Val Asp
290                     295                     300
Phe Leu Thr Asn Phe His Thr Asp Arg Ser Glu Asp Glu Gln Phe Asn
305                     310                     315                     320
Asp Glu Lys Ala Tyr Leu Ile Lys Gln Ile Lys Glu Leu Lys Pro Leu
325                     330                     335

    Pro Glu Ala
<210> SEQ ID NO 16
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: LKB1 substrate
<400> SEQUENCE: 16

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Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr
 20

<210> SEQ ID NO 17
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 17
 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20

<210> SEQ ID NO 18
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 18
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr
 20

<210> SEQ ID NO 19
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 19
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr
 20

<210> SEQ ID NO 20
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 20
 Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20

<210> SEQ ID NO 21
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 21
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15

Ser Leu Ala Tyr
20

<210> SEQ ID NO 22

<211> LENGTH: 375

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 22

Met Pro Leu Leu Phe Gly Lys Ser His Lys Ser Pro Ala Asp Val Val
1 5 10 15

Lys Thr Leu Arg Glu Val Leu Thr Ile Leu Asp Lys Leu Pro Pro Pro
20 25 30

Lys Leu Asp Lys Asp Gly Asn Ile Gln Ser Asp Lys Lys Tyr Asp Lys
35 40 45

Ala Leu Asp Glu Val Ser Lys Asn Val Ala Met Ile Lys Ser Phe Ile
50 55 60

Tyr Gly Asn Asp Ser Ala Glu Pro Ser Ser Glu His Val Val Gln Val
65 70 75 80

Ala Gln Leu Ala Gln Glu Val Tyr Asn Ala Asn Ile Leu Pro Met Leu
85 90 95

Ile Lys Met Leu Pro Lys Phe Glu Phe Glu Cys Lys Lys Asp Val Gly
100 105 110

Gln Ile Phe Asn Asn Leu Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
115 120 125

Thr Val Glu Tyr Leu Gly Ala Arg Pro Glu Ile Leu Ile Gln Leu Val
130 135 140

Gln Gly Tyr Ser Val Pro Asp Ile Ala Leu Thr Cys Gly Leu Met Leu
145 150 155 160

Arg Glu Ser Ile Arg His Asp His Leu Ala Lys Ile Ile Leu Tyr Ser
165 170 175

Asp Val Phe Tyr Thr Phe Phe Leu Tyr Val Gln Ser Glu Val Phe Asp
180 185 190

Ile Ser Ser Asp Ala Phe Ser Thr Phe Lys Glu Leu Thr Thr Arg His
195 200 205

Lys Ala Ile Ile Ala Glu Phe Leu Asp Ser Asn Tyr Asp Thr Phe Phe
210 215 220

Ala Gln Tyr Gln Asn Leu Leu Asn Ser Lys Asn Tyr Val Thr Arg Arg
225 230 235 240

Gln Ser Leu Lys Leu Leu Gly Glu Leu Leu Leu Asp Arg His Asn Phe
245 250 255

Asn Thr Met Thr Lys Tyr Ile Ser Asn Pro Asp Asn Leu Arg Leu Met
260 265 270

Met Glu Leu Leu Arg Asp Lys Ser Arg Asn Ile Gln Tyr Glu Ala Phe
275 280 285

His Val Phe Lys Val Phe Val Ala Asn Pro Asn Lys Pro Lys Pro Ile
290 295 300

Ser Asp Ile Leu Asn Arg Asn Arg Glu Lys Leu Val Glu Phe Leu Ser
305 310 315 320

Glu Phe His Asn Asp Arg Thr Asp Asp Glu Gln Phe Asn Asp Glu Lys
325 330 335

Ala Tyr Leu Ile Lys Gln Ile Gln Glu Met Lys Ser Ser Pro Lys Glu
340 345 350

Ala Lys Lys Pro Lys Ser Lys Glu Asp Glu Asn Gln Glu Pro Ala Gly
355 360 365

Pro Ser Glu Gly Pro Ser Thr Ser Gln
370 375

<210> SEQ ID NO 23

<211> LENGTH: 23

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: LKB1 substrate

<400> SEQUENCE: 23

Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
1 5 10 15
Ser Pro Leu Tyr Arg Arg Arg
20

<210> SEQ ID NO 24

<211> LENGTH: 19

<212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 24
 Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly Ser
 1 5 10 15
 Pro Leu Tyr
 <210> SEQ ID NO 25
 <211> LENGTH: 22
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 25
 Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly Ser
 1 5 10 15
 Pro Leu Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 26
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 26
 Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr
 20
 <210> SEQ ID NO 27
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 27
 Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 28
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 28
 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20
 <210> SEQ ID NO 29
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:

<223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 29
 Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 30
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 30
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr
 20
 <210> SEQ ID NO 31
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 31
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 32
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 32
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr
 20
 <210> SEQ ID NO 33
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 33
 Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
 1 5 10 15
 Ser Pro His Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 34
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 34

Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr
 20

<210> SEQ ID NO 35
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 35
 Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Pro Tyr Arg Arg Arg
 20

<210> SEQ ID NO 36
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 36
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15
 Ser Leu Ala Tyr
 20

<210> SEQ ID NO 37
 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: LKB1 substrate
 <400> SEQUENCE: 37
 Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
 1 5 10 15
 Ser Leu Ala Tyr Arg Arg Arg
 20

<210> SEQ ID NO 38
 <211> LENGTH: 19
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 38
 Met Val Ala Gly Leu Thr Leu Gly Lys Gly Pro Glu Ser Pro Asp Gly
 1 5 10 15
 Asp Val Ser

<210> SEQ ID NO 39
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 39
 Leu Ser Trp Gly Ala Gly Leu Lys Gly Gln Lys Val Ala Thr Ser Tyr
 1 5 10 15
 Glu Ser Ser Leu
 20

<210> SEQ ID NO 40
 <211> LENGTH: 21
 <212> TYPE: PRT

<213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 40
 Met Glu Gly Ala Ala Pro Val Ala Gly Asp Arg Pro Asp Leu Gly
 1 5 10 15
 Leu Gly Ala Pro Gly
 20
 <210> SEQ ID NO 41
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 41
 Thr Asp Cys Gln Glu Val Thr Ala Thr Tyr Arg Gln Ala Leu Arg Val
 1 5 10 15
 Cys Ser Lys Leu Thr
 20
 <210> SEQ ID NO 42
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 42
 Met Val Met Ala Asp Gly Pro Arg His Leu Gln Arg Gly Pro Val Arg
 1 5 10 15
 Val Gly Phe Tyr Asp
 20
 <210> SEQ ID NO 43
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 43
 Met Val Ile Met Ser Glu Phe Ser Ala Asp Pro Ala Gly Gln Gly Gln
 1 5 10 15
 Gly Gln Gln Lys
 20
 <210> SEQ ID NO 44
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 44
 Gly Asp Cys Glu Met Glu Asp Leu Met Pro Cys Ser Leu Gly Thr Phe
 1 5 10 15
 Val Leu Val Gln
 20
 <210> SEQ ID NO 45
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 45
 Thr Asp Ile Leu Leu Ser Tyr Lys His Pro Glu Val Ser Phe Ser Met
 1 5 10 15
 Glu Gln Ala Gly Val
 20
 <210> SEQ ID NO 46
 <211> LENGTH: 20
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 46
 Ser Gly Thr Ser Ile Ala Phe Lys Asn Ile Ala Ser Lys Ile Ala Asn


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      1           5           10           15
      Glu Leu Lys Leu
      20
<210> SEQ ID NO 47
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 47
      Met Ser Ser Arg Thr Val Leu Ala Pro Gly Asn Asp Arg Asn Ser Asp
      1           5           10           15
      Thr His Gly Thr
      20
<210> SEQ ID NO 48
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 48
      Met Lys Asp Tyr Asp Glu Leu Leu Lys Tyr Tyr Glu Leu His Glu Thr
      1           5           10           15
      Ile Gly Thr Gly
      20
<210> SEQ ID NO 49
<211> LENGTH: 16
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 49
      Cys Thr Ser Pro Pro Asp Ser Phe Leu Asp Asp His His Leu Thr Arg
      1           5           10           15
<210> SEQ ID NO 50
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 50
      Cys Asp Pro Met Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu
      1           5           10
<210> SEQ ID NO 51
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha
<400> SEQUENCE: 51
      Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Phe
      1           5           10
<210> SEQ ID NO 52
<211> LENGTH: 12
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, last residue
mutated to Ala
<400> SEQUENCE: 52
      Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Glu Ala
      1           5           10
<210> SEQ ID NO 53
<211> LENGTH: 12
<212> TYPE: PRT

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<213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, third last residue mutated t
 o Ala
 <400> SEQUENCE: 53
 Asn Leu Glu Glu Leu Glu Val Asp Asp Ala Glu Phe
 1 5 10
 <210> SEQ ID NO 54
 <211> LENGTH: 12
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 12 residues STRAD alpha, second last residue mutated t
 o Ala
 <400> SEQUENCE: 54
 Asn Leu Glu Glu Leu Glu Val Asp Asp Trp Ala Phe
 1 5 10
 <210> SEQ ID NO 55
 <211> LENGTH: 6
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: C-terminal 6 residues STRAD alpha
 <400> SEQUENCE: 55
 Val Asp Asp Trp Glu Phe
 1 5
 <210> SEQ ID NO 56
 <211> LENGTH: 547
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 56
 Met Ala Glu Pro Ser Gly Ser Pro Val His Val Gln Leu Pro Gln Gln
 1 5 10 15
 Ala Ala Pro Val Thr Ala Ala Ala Ala Ala Ala Pro Ala Ala Ala Thr
 20 25 30
 Ala Ala Pro Ala Pro Ala Ala Pro Ala Ala Pro Ala Pro Ala Pro Ala
 35 40 45
 Pro Ala Pro Ala Ala Gln Ala Val Gly Trp Pro Ile Cys Arg Asp Ala
 50 55 60
 Tyr Glu Leu Gln Glu Val Ile Gly Ser Gly Ala Thr Ala Val Val Gln
 65 70 75 80
 Ala Ala Leu Cys Lys Pro Arg Gln Glu Arg Val Ala Ile Lys Arg Ile
 85 90 95
 Asn Leu Glu Lys Cys Gln Thr Ser Met Asp Glu Leu Leu Lys Glu Ile
 100 105 110
 Gln Ala Met Ser Gln Cys Ser His Pro Asn Val Val Thr Tyr Tyr Thr
 115 120 125
 Ser Phe Val Val Lys Asp Glu Leu Trp Leu Val Met Lys Leu Leu Ser
 130 135 140
 Gly Gly Ser Met Leu Asp Ile Ile Lys Tyr Ile Val Asn Arg Gly Glu
 145 150 155 160
 His Lys Asn Gly Val Leu Glu Glu Ala Ile Ile Ala Thr Ile Leu Lys
 165 170 175
 Glu Val Leu Glu Gly Leu Asp Tyr Leu His Arg Asn Gly Gln Ile His
 180 185 190

Asn	Leu	Glu	Lys	Cys	Gln	Thr	Ser	Met	Asp	Glu	Leu	Leu	Lys	Glu	Ile	
50						55				60						
Gln	Ala	Met	Ser	Gln	Cys	His	His	Pro	Asn	Ile	Val	Ser	Tyr	Tyr	Thr	
65					70				75						80	
Ser	Phe	Val	Val	Lys	Asp	Glu	Leu	Trp	Leu	Val	Met	Lys	Leu	Leu	Ser	
				85					90					95		
Gly	Gly	Ser	Val	Leu	Asp	Ile	Ile	Lys	His	Ile	Val	Ala	Lys	Gly	Glu	
			100					105					110			
His	Lys	Ser	Gly	Val	Leu	Asp	Glu	Ser	Thr	Ile	Ala	Thr	Ile	Leu	Arg	
		115					120					125				
Glu	Val	Leu	Glu	Gly	Leu	Glu	Tyr	Leu	His	Lys	Asn	Gly	Gln	Ile	His	
	130					135					140					
Arg	Asp	Val	Lys	Ala	Gly	Asn	Ile	Leu	Leu	Gly	Glu	Asp	Gly	Ser	Val	
145					150					155					160	
Gln	Ile	Ala	Asp	Phe	Gly	Val	Ser	Ala	Phe	Leu	Ala	Thr	Gly	Gly	Asp	
				165					170					175		
Ile	Thr	Arg	Asn	Lys	Val	Arg	Lys	Thr	Phe	Val	Gly	Thr	Pro	Cys	Trp	
			180					185					190			
Met	Ala	Pro	Glu	Val	Met	Glu	Gln	Val	Arg	Gly	Tyr	Asp	Phe	Lys	Ala	
		195					200					205				
Asp	Ile	Trp	Ser	Phe	Gly	Ile	Thr	Ala	Ile	Glu	Leu	Ala	Thr	Gly	Ala	
	210					215					220					
Ala	Pro	Tyr	His	Lys	Tyr	Pro	Pro	Met	Lys	Val	Leu	Met	Leu	Thr	Leu	
225					230					235					240	
Gln	Asn	Asp	Pro	Pro	Ser	Leu	Glu	Thr	Gly	Val	Gln	Asp	Lys	Glu	Met	
				245					250					255		
Leu	Lys	Lys	Tyr	Gly	Lys	Ser	Phe	Arg	Lys	Met	Ile	Ser	Leu	Cys	Leu	
			260					265					270			
Gln	Lys	Asp	Pro	Glu	Lys	Arg	Pro	Thr	Ala	Ala	Glu	Leu	Arg	His		
		275					280					285				
Lys	Phe	Phe	Gln	Lys	Ala	Lys	Asn	Lys	Glu	Phe	Leu	Gln	Glu	Lys	Thr	
	290					295					300					
Leu	Gln	Arg	Ala	Pro	Thr	Ile	Ser	Glu	Arg	Ala	Lys	Lys	Val	Arg	Arg	
305					310					315					320	
Val	Pro	Gly	Ser	Ser	Gly	Arg	Leu	His	Lys	Thr	Glu	Asp	Gly	Gly	Trp	
				325					330					335		
Glu	Trp	Ser	Asp	Asp	Glu	Phe	Asp	Glu	Glu	Ser	Glu	Glu	Gly	Lys	Ala	
			340					345					350			
Ala	Ile	Ser	Gln	Leu	Arg	Ser	Pro	Arg	Val	Lys	Glu	Ser	Ile	Ser	Asn	
		355					360					365				
Ser	Glu	Leu	Phe	Pro	Thr	Thr	Asp	Pro	Val	Gly	Thr	Leu	Leu	Gln	Val	
	370					375					380					
Pro	Glu	Gln	Ile	Ser	Ala	His	Leu	Pro	Gln	Pro	Ala	Gly	Gln	Ile	Ala	
385					390					395					400	
Thr	Gln	Pro	Thr	Gln	Val	Ser	Leu	Pro	Pro	Thr	Ala	Glu	Pro	Ala	Lys	
				405					410					415		
Thr	Ala	Gln	Ala	Leu	Ser	Ser	Gly	Ser	Gly	Ser	Gln	Glu	Thr	Lys	Ile	
			420				425						430			
Pro	Ile	Ser	Leu	Val	Leu	Arg	Leu	Arg	Asn	Ser	Lys	Lys	Glu	Leu	Asn	
		435					440					445				
Asp	Ile	Arg	Phe	Glu	Phe	Thr	Pro	Gly	Arg	Asp	Thr	Ala	Glu	Gly	Val	
	450					455					460					
Ser	Gln	Glu	Leu	Ile	Ser	Ala	Gly	Leu	Val	Asp	Gly	Arg	Asp	Leu	Val	
465					470					475					480	
Ile	Val	Ala	Ala	Asn	Leu	Gln	Lys	Ile	Val	Glu	Glu	Pro	Gln	Ser	Asn	
				485					490					495		
Arg	Ser	Val	Thr	Phe	Lys	Leu	Ala	Ser	Gly	Val	Glu	Gly	Ser	Asp	Ile	

				500						505					510
	Pro	Asp	Asp	Gly	Lys	Leu	Ile	Gly	Phe	Ala	Gln	Leu	Ser	Ile	Ser
				515				520					525		

<210> SEQ ID NO 58
 <211> LENGTH: 560
 <212> TYPE: PRT
 <213> ORGANISM: *Saccharomyces cerevisiae*
 <400> SEQUENCE: 58

Met	Val	Leu	Leu	Lys	Glu	Pro	Val	Gln	Pro	Leu	Pro	Arg	Ser	Ser	Leu
1				5					10					15	
Leu	Tyr	Asn	Asn	Ala	Ser	Asn	Ser	Ser	Ser	Arg	Ile	Lys	Glu	Thr	Arg
			20					25					30		
Lys	Val	Lys	Leu	Leu	Tyr	Asn	Pro	Leu	Thr	Lys	Arg	Gln	Ile	Leu	Asn
		35					40					45			
Asn	Phe	Glu	Ile	Leu	Ala	Thr	Leu	Gly	Asn	Gly	Gln	Tyr	Gly	Lys	Val
	50					55					60				
Lys	Leu	Ala	Arg	Asp	Leu	Gly	Thr	Gly	Ala	Leu	Val	Ala	Ile	Lys	Ile
65					70					75				80	
Leu	Asn	Arg	Phe	Glu	Lys	Arg	Ser	Gly	Tyr	Ser	Leu	Gln	Leu	Lys	Val
				85					90					95	
Glu	Asn	Pro	Arg	Val	Asn	Gln	Glu	Ile	Glu	Val	Met	Lys	Arg	Cys	His
			100					105					110		
His	Glu	Asn	Val	Val	Glu	Leu	Tyr	Glu	Ile	Leu	Asn	Asp	Pro	Glu	Ser
		115						120				125			
Thr	Lys	Val	Tyr	Leu	Val	Leu	Glu	Tyr	Cys	Ser	Arg	Gly	Pro	Val	Lys
	130					135						140			
Trp	Cys	Pro	Glu	Asn	Lys	Met	Glu	Ile	Lys	Ala	Val	Gly	Pro	Ser	Ile
145					150					155					160
Leu	Thr	Phe	Gln	Gln	Ser	Arg	Lys	Val	Val	Leu	Asp	Val	Val	Ser	Gly
			165						170					175	
Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Ile	Thr	His	Arg	Asp	Ile	Lys	Pro
			180					185					190		
Ser	Asn	Leu	Leu	Ile	Ser	Ser	Asn	Gly	Thr	Val	Lys	Ile	Ser	Asp	Phe
		195					200					205			
Gly	Val	Ala	Met	Ser	Thr	Ala	Thr	Gly	Ser	Thr	Asn	Ile	Gln	Ser	Ser
	210					215					220				
His	Glu	Gln	Leu	Leu	Lys	Ser	Arg	Ala	Leu	Gly	Thr	Pro	Ala	Phe	Phe
225					230					235				240	
Ala	Pro	Glu	Leu	Cys	Ser	Thr	Glu	Lys	Glu	Tyr	Ser	Cys	Ser	Ser	Ala
				245					250					255	
Ile	Asp	Ile	Trp	Ser	Leu	Gly	Val	Thr	Ile	Tyr	Cys	Leu	Leu	Phe	Gly
			260					265					270		
Lys	Leu	Pro	Phe	Asn	Ala	Asn	Ser	Gly	Leu	Glu	Leu	Phe	Asp	Ser	Ile
		275					280					285			
Ile	Asn	Lys	Pro	Leu	Glu	Phe	Pro	Ser	Tyr	Glu	Glu	Met	Leu	Asn	Gly
	290					295					300				
Ala	Thr	Ser	Gly	Ile	Thr	Met	Glu	Glu	Tyr	Thr	Asp	Ala	Lys	Asp	Leu
305					310					315				320	
Leu	Lys	Lys	Leu	Leu	Gln	Lys	Asp	Pro	Asp	Lys	Arg	Ile	Lys	Leu	Ala
				325					330					335	
Asp	Ile	Lys	Val	His	Pro	Phe	Met	Cys	His	Tyr	Gly	Lys	Ser	Asp	Ala
			340					345					350		
Ala	Ser	Val	Leu	Thr	Asn	Leu	Glu	Thr	Phe	His	Glu	Leu	Lys	Val	Ser
		355					360					365			
Pro	Pro	Ser	Ser	Cys	Lys	Arg	Val	Glu	Leu	Val	Ser	Leu	Pro	Val	Asn
	370					375					380				
Ser	Ser	Phe	Ala	Ser	Leu	Asp	Ser	Val	Tyr	Met	Glu	Asn	Phe	Asp	His

385	Asn	Asn	Leu	Arg	Thr	Gly	Ala	Asp	Arg	Asn	Ser	Thr	Tyr	Ser	Pro	Ser
					405					410					415	
Ile	Tyr	Asp	Ala	Asn	Thr	Leu	Ser	Pro	Ser	Ala	Tyr	His	Asn	Ile	Gly	
			420					425					430			
Ser	Arg	Glu	Ser	Ser	Tyr	Ser	Ser	Phe	Ser	Ser	Phe	Thr	Ser	Ser	Thr	
		435					440				445					
Ala	Phe	Ala	Ser	Gln	Ile	Ser	Ile	Gln	Asp	Ala	Pro	Ala	Ile	Gly	Asp	
	450					455				460						
Gln	Gln	Cys	Leu	Ile	Gly	Glu	Ser	Gly	Ser	Ser	Leu	Arg	Val	Asn	Ser	
465					470					475				480		
Cys	Glu	Phe	Pro	Gln	Tyr	Thr	Thr	Met	Ser	Pro	Val	Gly	Glu	Tyr	Pro	
				485					490				495			
Phe	Glu	Ser	Thr	Glu	Ala	Ser	Leu	Ser	Ser	Thr	Leu	Thr	Pro	Val	Gly	
			500					505				510				
Asn	Val	Pro	Gln	Arg	Ile	Lys	Ala	His	Leu	Val	Glu	Gly	Lys	Ser	Asn	
		515					520					525				
Ser	Lys	Asp	Asp	Leu	Arg	Ile	Glu	Ala	Asp	Ala	Ser	Leu	Val	Phe	Glu	
	530					535				540						
Ala	Ser	Asp	Ala	Gln	Arg	Thr	Arg	Arg	Arg	Met	Ser	Leu	Tyr	Lys	Leu	
545				550				555							560	

<210> SEQ ID NO 59

<211> LENGTH: 1142

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 59

Met	Asp	Arg	Ser	Asp	Lys	Lys	Val	Asn	Val	Glu	Glu	Val	Asn	Val	Pro
1			5					10					15		
Ser	Asn	Leu	Gln	Ile	Glu	Leu	Glu	Lys	Ser	Gly	Thr	Ser	Ser	Ser	Val
		20					25					30			
Ser	Leu	Arg	Ser	Pro	Thr	Lys	Ser	Ser	Ala	Thr	Asn	Leu	Ala	Gly	Met
	35					40					45				
Ala	Glu	Gly	Ala	Arg	Asp	Asn	Ala	Ser	Ile	Ala	Ser	Ser	Ser	Val	Asp
	50					55				60					
Ser	Leu	Asn	Met	Leu	Leu	Glu	Arg	Gln	Arg	Val	Arg	Gln	Leu	Asn	His
65				70					75				80		
Pro	Gln	His	Gln	Gln	His	Ile	Ser	Ser	Ser	Leu	Ala	Lys	Thr	Pro	Thr
			85					90					95		
Thr	Thr	Ser	Ser	Phe	Cys	Ser	Ser	Gly	Ser	Ser	Lys	Asn	Lys	Val	Lys
		100					105					110			
Glu	Thr	Asn	Arg	Ile	Ser	Leu	Thr	Tyr	Asp	Pro	Val	Ser	Lys	Arg	Lys
		115					120				125				
Val	Leu	Asn	Thr	Tyr	Glu	Ile	Ile	Lys	Glu	Leu	Gly	His	Gly	Gln	His
	130					135				140					
Gly	Lys	Val	Lys	Leu	Ala	Arg	Asp	Ile	Leu	Ser	Lys	Gln	Leu	Val	Ala
145				150					155				160		
Ile	Lys	Ile	Val	Asp	Arg	His	Glu	Lys	Lys	Gln	Arg	Lys	Phe	Phe	Thr
			165					170					175		
Phe	Ile	Lys	Ser	Ser	Lys	Ile	Ser	Glu	Asn	Asp	Lys	Ile	Lys	Arg	Glu
		180					185					190			
Ile	Ala	Ile	Met	Lys	Lys	Cys	His	His	Lys	His	Val	Val	Gln	Leu	Ile
	195					200					205				
Glu	Val	Leu	Asp	Asp	Leu	Lys	Ser	Arg	Lys	Ile	Tyr	Leu	Val	Leu	Glu
	210				215					220					
Tyr	Cys	Ser	Arg	Gly	Glu	Val	Lys	Trp	Cys	Pro	Pro	Asp	Cys	Met	Glu
225				230					235				240		
Ser	Asp	Ala	Lys	Gly	Pro	Ser	Leu	Leu	Ser	Phe	Gln	Glu	Thr	Arg	Glu

Ile	Leu	Arg	Gly	Val	Val	Leu	Gly	Leu	Glu	Tyr	Leu	His	Tyr	Gln	Gly
			260						265					270	
Ile	Ile	His	Arg	Asp	Ile	Lys	Pro	Ala	Asn	Leu	Leu	Ile	Ser	Gly	Asp
		275					280					285			
Gly	Thr	Val	Lys	Ile	Ser	Asp	Phe	Gly	Val	Ser	Leu	Ala	Ala	Ser	Ser
	290					295					300				
Thr	Asn	Ser	Ser	Asp	Ser	Ser	Glu	Ser	Leu	Asp	Glu	Leu	Glu	Leu	Ala
305					310					315					320
Lys	Thr	Val	Gly	Thr	Pro	Ala	Phe	Phe	Ala	Pro	Glu	Met	Cys	Leu	Gly
			325						330					335	
Glu	Asp	Ala	Phe	Thr	Arg	Tyr	Asn	Leu	Thr	Lys	Glu	Asn	Leu	Phe	Arg
		340					345					350			
Gly	Ser	Cys	Ile	Ser	Phe	Met	Ile	Asp	Ile	Trp	Ala	Val	Gly	Val	Thr
	355						360				365				
Leu	Tyr	Cys	Leu	Leu	Phe	Gly	Met	Leu	Pro	Phe	Phe	Ser	Asp	Phe	Glu
	370					375					380				
Leu	Lys	Leu	Phe	Glu	Lys	Ile	Val	Asn	Asp	Pro	Leu	Lys	Phe	Pro	Thr
385					390				395						400
Phe	Lys	Glu	Ile	Gln	Ser	Asn	Lys	Val	Ser	Lys	Val	Ser	Cys	Glu	Glu
			405					410						415	
Glu	Tyr	Glu	Met	Ala	Lys	Asp	Leu	Leu	Leu	Lys	Leu	Leu	Glu	Lys	Asn
			420				425					430			
Pro	Gln	Lys	Arg	Met	Thr	Ile	Pro	Ala	Ile	Lys	Lys	His	Pro	Phe	Val
	435						440					445			
Ser	Trp	Asp	Phe	Asp	His	Val	Pro	Glu	Asn	Asp	Glu	Lys	Leu	Leu	Ser
	450					455					460				
Ser	Val	Leu	Glu	Gln	Lys	Leu	Arg	Phe	Gln	Cys	Asn	Gln	Thr	Asp	Gln
465					470				475						480
Phe	Glu	Pro	Ile	Ser	Ile	Ser	Lys	His	Glu	Leu	Lys	Asn	Ala	Val	Ser
			485						490					495	
Gly	Val	Gly	Lys	Lys	Ile	Lys	Glu	Ser	Val	Leu	Lys	Ser	Ile	Pro	Leu
			500				505						510		
Lys	Asp	Pro	Ser	Asp	Leu	Ser	Asn	Lys	Asn	Tyr	Leu	His	Pro	Thr	Glu
	515						520					525			
Thr	Thr	Arg	Gly	Arg	Gly	Asp	Ala	Asn	Val	Ile	Val	Ser	Glu	Gly	Ser
	530					535					540				
Val	Leu	Ser	Asn	Ile	Lys	Glu	Leu	Ser	Ala	Asn	Asp	Gly	Cys	Leu	Asn
545					550				555						560
Thr	Asp	Ser	Asp	Thr	Asn	Ile	Asn	Ile	Asn	Asp	Asp	Asp	His	Tyr	Ser
			565					570					575		
Gly	Asp	Asp	Asn	Asp	Gly	His	Leu	Thr	Lys	Arg	Glu	Leu	Glu	Arg	Glu
			580				585					590			
Leu	Asn	Lys	Phe	Asp	Asp	Lys	His	Glu	Ala	Gly	Asn	Met	Val	Asn	Leu
	595						600					605			
Pro	Ile	Asn	Ser	Ser	Phe	Ala	Ser	Leu	Asp	Ser	Phe	Tyr	Ile	Asp	Asn
	610					615					620				
Phe	Ala	Met	Ala	Arg	Met	Gly	Met	Ser	Ser	Pro	Glu	Ala	Gly	Asp	Ser
625					630					635					640
Val	Ser	Ser	Val	Pro	Asn	Leu	Pro	Ser	Ala	Pro	Ser	Ser	Thr	Arg	Leu
			645						650					655	
Gly	Arg	Ser	Pro	Val	Phe	Ser	Gly	Val	Thr	Asn	Gln	Pro	Ser	Pro	Ile
			660				665					670			
Arg	Pro	Val	Leu	Pro	Gln	Gln	Lys	Ser	Ser	Phe	Cys	Ala	Thr	Gly	Arg
	675						680					685			
Tyr	Asp	Lys	Ser	His	Asn	Ser	Leu	Leu	Arg	Asn	Ser	Ser	Ser	His	Leu
	690					695					700				

Thr	Ser	Tyr	Asn	Ser	Gly	Arg	Pro	Ser	Ser	Arg	Thr	Gly	Arg	Met	Asn	
705					710					715					720	
Ser	Arg	Asn	Gln	Asn	Leu	Pro	Lys	Ile	Pro	Asn	Ser	Leu	Ser	Lys	Ile	
				725					730					735		
Ser	Thr	Thr	Lys	Leu	Thr	Glu	Leu	Arg	Val	Pro	Lys	Asp	Ser	Glu	Ile	
			740					745				750				
Pro	Ser	Pro	Ala	Lys	Asn	Pro	Asn	Ala	Asp	Arg	Leu	Arg	Arg	Phe	Pro	
		755					760				765					
Val	Lys	Lys	Asn	Thr	Lys	Thr	Pro	Ala	Ile	Lys	Asp	Pro	Pro	Arg	Ile	
	770					775					780					
Asn	Ile	Asn	Ser	Ser	Asp	Lys	Ser	Gly	Ser	Lys	Asn	Ser	Pro	Ile	Lys	
785					790					795					800	
Ser	Leu	Tyr	Gln	Arg	Met	Lys	Gln	Ser	Lys	Asp	Asn	Ser	Lys	Thr	Phe	
				805					810					815		
Glu	Val	Arg	Arg	Gly	Asn	Phe	Phe	Ser	His	Phe	Asn	Gly	Asp	Asp	Asp	
			820					825					830			
Asp	Ser	Ser	Ser	Gln	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ser	Glu	Ser	Asp	
		835					840					845				
Ser	Glu	Leu	Ser	Ser	Thr	Ser	Ser	Ser	Cys	Thr	Ser	Gly	Thr	Gln	Ser	
	850					855					860					
Arg	Asn	Ser	Ser	Asn	Asn	Asn	Ala	Tyr	Ser	Glu	Thr	Glu	Ser	Leu	Pro	
865					870					875					880	
Phe	Glu	Phe	Gly	Val	Asp	Ser	Glu	Asp	Gly	Ser	Gly	Val	Leu	Leu	Arg	
			885						890					895		
Asp	Leu	Pro	Asn	Glu	Asp	Gln	Ile	Arg	Pro	Phe	Leu	Asp	Ile	Gln	Pro	
		900						905					910			
Cys	Arg	Arg	Met	Lys	Val	Lys	Ser	Ser	Leu	Asn	Leu	Glu	Pro	Pro	Ser	
	915						920					925				
Val	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Ser	Asp	Glu	Asp	Glu	Leu	Ile	Leu	
	930					935					940					
Asn	Val	Gly	Thr	Ala	Gly	His	Arg	Arg	Arg	His	Asn	Ser	Ser	Lys	Leu	
945					950					955					960	
Ser	Glu	Leu	Ser	Asn	Ser	Pro	Gln	Lys	Gly	Ser	Asn	Asn	Phe	Met	Tyr	
			965						970					975		
Ser	Asn	Gly	Ser	Val	His	Asp	Ser	Glu	Thr	Thr	Ile	Thr	Pro	Gln	Asn	
		980						985					990			
Met	Asp	Asp	Leu	Thr	Leu	His	Gln	Ala	Leu	Ser	Arg	Ser	Gln	Pro	Ile	
	995						1000						1005			
Ser	Lys	Pro	Gly	Pro	Leu	Val	Leu	Pro	Lys	Arg	Leu	Asp	Gln	Lys		
	1010					1015					1020					
Lys	Ala	Thr	Thr	Glu	Thr	Ser	Asn	Leu	Thr	Asp	Ile	Val	Glu	Phe		
	1025					1030					1035					
Asn	Gly	Asn	Asn	Asp	His	Arg	Lys	Asp	Lys	Asn	Phe	Asp	Lys	Val		
	1040					1045					1050					
Leu	Tyr	Ser	Arg	Asp	Leu	Leu	Lys	Asp	Ala	Leu	Ser	Ser	Thr	Asn		
	1055					1060					1065					
Ala	Gly	Arg	Arg	Arg	Ser	Ile	Pro	Ser	Asn	Lys	Ile	Arg	Gly	Arg		
	1070					1075					1080					
Lys	Asp	Ala	Ser	Ile	Thr	Met	Ser	Thr	Asn	Val	Gly	Asn	Asp	Glu		
	1085					1090					1095					
His	Ala	Arg	Asn	Thr	Ser	Cys	His	Gly	Asp	Lys	Gly	Gln	Glu	Asn		
	1100					1105					1110					
Gly	Ala	Ile	Lys	Gln	Arg	Thr	His	Glu	Arg	Ser	Arg	Ser	Leu	Thr		
	1115					1120					1125					
Val	Ala	Glu	Leu	Asn	Glu	Glu	Lys	Arg	Arg	Ser	Ala	Leu	Pro			
	1130					1135					1140					

<211> LENGTH: 640

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 60

Met	Ser	Pro	Arg	Gln	Leu	Ile	Pro	Thr	Leu	Ile	Pro	Glu	Trp	Ala	Pro	
1				5					10					15		
Leu	Ser	Gln	Gln	Ser	Cys	Ile	Arg	Glu	Asp	Glu	Leu	Asp	Ser	Pro	Pro	
		20						25					30			
Ile	Thr	Pro	Thr	Ser	Gln	Thr	Ser	Phe	Gly	Ser	Ser	Phe	Ser	Gln		
	35					40				45						
Gln	Lys	Pro	Thr	Tyr	Ser	Thr	Ile	Ile	Gly	Glu	Asn	Ile	His	Thr	Ile	
50						55				60						
Leu	Asp	Glu	Ile	Arg	Pro	Tyr	Val	Lys	Lys	Ile	Thr	Val	Ser	Asp	Gln	
65				70						75					80	
Asp	Lys	Lys	Thr	Ile	Asn	Gln	Tyr	Thr	Leu	Gly	Val	Ser	Ala	Gly	Ser	
			85						90					95		
Gly	Gln	Phe	Gly	Tyr	Val	Arg	Lys	Ala	Tyr	Ser	Ser	Thr	Leu	Gly	Lys	
		100						105					110			
Val	Val	Ala	Val	Lys	Ile	Ile	Pro	Lys	Lys	Pro	Trp	Asn	Ala	Gln	Gln	
		115					120					125				
Tyr	Ser	Val	Asn	Gln	Val	Met	Arg	Gln	Ile	Gln	Leu	Trp	Lys	Ser	Lys	
130						135					140					
Gly	Lys	Ile	Thr	Thr	Asn	Met	Ser	Gly	Asn	Glu	Ala	Met	Arg	Leu	Met	
145					150					155					160	
Asn	Ile	Glu	Lys	Cys	Arg	Trp	Glu	Ile	Phe	Ala	Ala	Ser	Arg	Leu	Arg	
				165					170					175		
Asn	Asn	Val	His	Ile	Val	Arg	Leu	Ile	Glu	Cys	Leu	Asp	Ser	Pro	Phe	
		180						185					190			
Ser	Glu	Ser	Ile	Trp	Ile	Val	Thr	Asn	Trp	Cys	Ser	Leu	Gly	Glu	Leu	
	195						200					205				
Gln	Trp	Lys	Arg	Asp	Asp	Asp	Glu	Asp	Ile	Leu	Pro	Gln	Trp	Lys	Lys	
210					215						220					
Ile	Val	Ile	Ser	Asn	Cys	Ser	Val	Ser	Thr	Phe	Ala	Lys	Lys	Ile	Leu	
225				230						235					240	
Glu	Asp	Met	Thr	Lys	Gly	Leu	Glu	Tyr	Leu	His	Ser	Gln	Gly	Cys	Ile	
			245						250					255		
His	Arg	Asp	Ile	Lys	Pro	Ser	Asn	Ile	Leu	Leu	Asp	Glu	Glu	Glu	Lys	
		260						265					270			
Val	Ala	Lys	Leu	Ser	Asp	Phe	Gly	Ser	Cys	Ile	Phe	Thr	Pro	Gln	Ser	
		275					280					285				
Leu	Pro	Phe	Ser	Asp	Ala	Asn	Phe	Glu	Asp	Cys	Phe	Gln	Arg	Glu	Leu	
290					295						300					
Asn	Lys	Ile	Val	Gly	Thr	Pro	Ala	Phe	Ile	Ala	Pro	Glu	Leu	Cys	His	
305				310					315						320	
Leu	Gly	Asn	Ser	Lys	Arg	Asp	Phe	Val	Thr	Asp	Gly	Phe	Lys	Leu	Asp	
			325						330					335		
Ile	Trp	Ser	Leu	Gly	Val	Thr	Leu	Tyr	Cys	Leu	Leu	Tyr	Asn	Glu	Leu	
		340						345					350			
Pro	Phe	Phe	Gly	Glu	Asn	Glu	Phe	Glu	Thr	Tyr	His	Lys	Ile	Ile	Glu	
	355						360					365				
Val	Ser	Leu	Ser	Ser	Lys	Ile	Asn	Gly	Asn	Thr	Leu	Asn	Asp	Leu	Val	
	370					375					380					
Ile	Lys	Arg	Leu	Leu	Glu	Lys	Asp	Val	Thr	Leu	Arg	Ile	Ser	Ile	Gln	
385				390					395						400	
Asp	Leu	Val	Lys	Val	Leu	Ser	Arg	Asp	Gln	Pro	Ile	Asp	Ser	Arg	Asn	
			405						410					415		
His	Ser	Gln	Ile	Ser	Ser	Ser	Ser	Val	Asn	Pro	Val	Arg	Asn	Glu	Gly	

195	200	205
Arg Arg Pro Pro Pro Arg Gly Thr Arg Pro Ala Pro Gly Gly Cys Ile		
210	215	220
Gln Pro Arg Gly Pro Ile Glu Gln Val Tyr Gln Glu Ile Ala Ile Leu		
225	230	235
Lys Lys Leu Asp His Pro Asn Val Val Lys Leu Val Glu Val Leu Asp		240
	245	250
Asp Pro Asn Glu Asp His Leu Tyr Met Val Phe Glu Leu Val Asn Gln		255
	260	265
Gly Pro Val Met Glu Val Pro Thr Leu Lys Pro Leu Ser Glu Asp Gln		270
	275	280
Ala Arg Phe Tyr Phe Gln Asp Leu Ile Lys Gly Ile Glu Tyr Leu His		285
	290	295
Tyr Gln Lys Ile Ile His Arg Asp Ile Lys Pro Ser Asn Leu Leu Val		300
305	310	315
Gly Glu Asp Gly His Ile Lys Ile Ala Asp Phe Gly Val Ser Asn Glu		320
	325	330
Phe Lys Gly Ser Asp Ala Leu Leu Ser Asn Thr Val Gly Thr Pro Ala		335
	340	345
Phe Met Ala Pro Glu Ser Leu Ser Glu Thr Arg Lys Ile Phe Ser Gly		350
	355	360
Lys Ala Leu Asp Val Trp Ala Met Gly Val Thr Leu Tyr Cys Phe Val		365
	370	375
Phe Gly Gln Cys Pro Phe Met Asp Glu Arg Ile Met Cys Leu His Ser		380
385	390	395
Lys Ile Lys Ser Gln Ala Leu Glu Phe Pro Asp Gln Pro Asp Ile Ala		400
	405	410
Glu Asp Leu Lys Asp Leu Ile Thr Arg Met Leu Asp Lys Asn Pro Glu		415
	420	425
Ser Arg Ile Val Val Pro Glu Ile Lys Ile Leu Val Lys Thr Met Ile		430
	435	440
Arg Lys Arg Ser Phe Gly Asn Pro Phe Glu Gly Ser Arg Arg Glu Glu		445
	450	455
Arg Ser Leu Ser Ala Pro Gly Asn Leu Leu Thr Lys Lys Pro Thr Arg		460
465	470	475
Glu Cys Glu Ser Leu Ser Glu Leu Lys Glu Ala Arg Gln Arg Arg Gln		480
	485	490
Pro Pro Gly His Arg Pro Ala Pro Arg Gly Gly Gly Gly Ser Ala Leu		495
	500	505
Val Arg Gly Ser Pro Cys Val Glu Ser Cys Trp Ala Pro Ala Pro Gly		510
	515	520
Ser Pro Ala Arg Met His Pro Leu Arg Pro Glu Glu Ala Met Glu Pro		525
	530	535
		540
Glu		
545		

<210> SEQ ID NO 62

<211> LENGTH: 243

<212> TYPE: PRT

<213> ORGANISM: Artificial

<220> FEATURE:

<223> OTHER INFORMATION: Consensus for figure 12

<400> SEQUENCE: 62

Pro Ser Ser Ser Ser Ser Ser Arg Ile Lys Thr Val Leu Tyr Pro Leu		
1	5	10
Thr Lys Arg Gln Ile Leu Asn Asn Tyr Ile Leu Gly Gly Gln Tyr Gly		15
	20	25
Lys Val Lys Leu Ala Asp Thr Leu Val Ala Ile Lys Ile Leu Lys Lys		30

<400> SEQUENCE: 66
 Asp Phe Gly Leu Ser Asn Tyr His Gln Gly Lys Phe Leu Gln Thr Phe
 1 5 10 15
 Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu
 20 25

<210> SEQ ID NO 67
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 67
 Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr
 1 5 10 15
 Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu
 20 25

<210> SEQ ID NO 68
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 68
 Asp Phe Gly Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr
 1 5 10 15
 Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu
 20 25

<210> SEQ ID NO 69
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 69
 Asp Phe Gly Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr
 1 5 10 15
 Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 70
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens

<400> SEQUENCE: 70
 Asp Phe Gly Phe Gly Asn Phe Phe Lys Ser Gly Glu Leu Leu Ala Thr
 1 5 10 15
 Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 71
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 71
 Asp Phe Gly Leu Ser Asn Ile Met Arg Asp Gly His Phe Leu Lys Thr
 1 5 10 15
 Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 72
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Arabidopsis thaliana

<400> SEQUENCE: 72
 Asp Phe Gly Leu Ser Asn Val Met Arg Asp Gly His Phe Leu Lys Thr
 1 5 10 15

Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 73
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 73
 Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr
 1 5 10 15
 Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 74
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 74
 Asp Phe Gly Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr
 1 5 10 15
 Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 75
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Saccharomyces cerevisiae
 <400> SEQUENCE: 75
 Asp Phe Gly Leu Ser Asn Ile Met Thr Asp Gly Asn Phe Leu Lys Thr
 1 5 10 15
 Ser Cys Gly Ser Pro Asn Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 76
 <211> LENGTH: 27
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 76
 Asp Phe Gly Phe Ser Asn Leu Phe Thr Pro Gly Gln Leu Leu Lys Thr
 1 5 10 15
 Trp Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 77
 <211> LENGTH: 29
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 77
 Asp Phe Gly Leu Cys Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu
 1 5 10 15
 Gln Thr Cys Cys Gly Ser Leu Ala Tyr Ala Ala Pro Glu
 20 25

<210> SEQ ID NO 78
 <211> LENGTH: 21
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: consensus from figure 19
 <400> SEQUENCE: 78
 Asp Phe Gly Leu Ser Asn Leu Gly Phe Leu Thr Ser Cys Gly Ser Pro
 1 5 10 15
 Tyr Ala Ala Pro Glu

20

<210> SEQ ID NO 79
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 79
Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr
1 5 10 15
Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 80
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 80
Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Asn Lys Leu Asp Thr
1 5 10 15
Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 81
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 81
Asp Phe Gly Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr
1 5 10 15
Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 82
<211> LENGTH: 27
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 82
Asp Phe Gly Phe Ser Asn Glu Phe Thr Leu Gly Ser Lys Leu Asp Thr
1 5 10 15
Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu
20 25

<210> SEQ ID NO 83
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 83
Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
1 5 10 15
Ser Pro Leu Tyr Arg Arg Arg
20

<210> SEQ ID NO 84
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 84
Phe Gly Asn Phe Tyr Lys Ser Gly Glu Pro Leu Ser Thr Trp Cys Gly
1 5 10 15
Ser Pro Pro Tyr Arg Arg Arg
20

<210> SEQ ID NO 85
<211> LENGTH: 23

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<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 85
Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
1           5           10           15
Ser Pro Asn Tyr Arg Arg Arg
                20

<210> SEQ ID NO 86
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 86
Met Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly
1           5           10           15
Ser Pro His Tyr Arg Arg Arg
                20

<210> SEQ ID NO 87
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 87
Phe Ser Asn Glu Phe Thr Val Gly Gly Lys Leu Asp Thr Phe Cys Gly
1           5           10           15
Ser Pro Pro Tyr Arg Arg Arg
                20

<210> SEQ ID NO 88
<211> LENGTH: 23
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 88
Ala Lys Pro Lys Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly
1           5           10           15
Ser Leu Ala Tyr Arg Arg Arg
                20

<210> SEQ ID NO 89
<211> LENGTH: 32
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 89
Ile Ala Ala Phe Gly Ala Ser Leu Gln Val Gly Asp Ser Leu Leu Glu
1           5           10           15
Thr Ser Cys Gly Ser Pro His Tyr Ala Cys Pro Glu Arg Val Ile Arg
                20           25           30

<210> SEQ ID NO 90
<211> LENGTH: 25
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 90
Ser Leu Gln Val Gly Asp Ser Leu Leu Glu Thr Ser Cys Gly Ser Pro
1           5           10           15
His Tyr Ala Cys Pro Glu Val Ile Arg
                20           25

<210> SEQ ID NO 91
<211> LENGTH: 20
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 91

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Phe Leu Gln Thr Phe Cys Gly Ser Pro Leu Tyr Ala Ser Pro Glu Ile
 1 5 10 15
 Val Asn Gly Lys
 20

<210> SEQ ID NO 92

<211> LENGTH: 19

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 92

Leu Asp Thr Phe Cys Gly Ser Pro Pro Tyr Ala Ala Pro Glu Leu Phe
 1 5 10 15
 Gln Gly Lys

<210> SEQ ID NO 93

<211> LENGTH: 25

<212> TYPE: PRT

<213> ORGANISM: Homo sapiens

<400> SEQUENCE: 93

Gly Asn Lys Asp Tyr His Leu Gln Thr Cys Cys Gly Ser Leu Ala Tyr
 1 5 10 15
 Ala Ala Pro Glu Leu Ile Gln Cys Lys
 20 25

<210> SEQ ID NO 94

<211> LENGTH: 329

<212> TYPE: PRT

<213> ORGANISM: Schizosaccharomyces pombe

<400> SEQUENCE: 94

Met Ser Phe Leu Phe Asn Lys Arg Pro Lys Ser Thr Gln Asp Val Val
 1 5 10 15
 Arg Cys Leu Cys Asp Asn Leu Pro Lys Leu Glu Ile Asn Asn Asp Lys
 20 25 30
 Lys Lys Ser Phe Glu Glu Val Ser Lys Cys Leu Gln Asn Leu Arg Val
 35 40 45
 Ser Leu Cys Gly Thr Ala Glu Val Glu Pro Asp Ala Asp Leu Val Ser
 50 55 60
 Asp Leu Ser Phe Gln Ile Tyr Gln Ser Asn Leu Pro Phe Leu Leu Val
 65 70 75 80
 Arg Tyr Leu Pro Lys Leu Glu Phe Glu Ser Lys Lys Asp Thr Gly Leu
 85 90 95
 Ile Phe Ser Ala Leu Leu Arg Arg His Val Ala Ser Arg Tyr Pro Thr
 100 105 110
 Val Asp Tyr Met Leu Ala His Pro Gln Ile Phe Pro Val Leu Val Ser
 115 120 125
 Tyr Tyr Arg Tyr Gln Glu Val Ala Phe Thr Ala Gly Ser Ile Leu Arg
 130 135 140
 Glu Cys Ser Arg His Glu Ala Leu Asn Glu Val Leu Leu Asn Ser Arg
 145 150 155 160
 Asp Phe Trp Thr Phe Phe Ser Leu Ile Gln Ala Ser Ser Phe Asp Met
 165 170 175
 Ala Ser Asp Ala Phe Ser Thr Phe Lys Ser Ile Leu Leu Asn His Lys
 180 185 190
 Ser Gln Val Ala Glu Phe Ile Ser Tyr His Phe Asp Glu Phe Phe Lys
 195 200 205
 Gln Tyr Thr Val Leu Leu Lys Ser Glu Asn Tyr Val Thr Lys Arg Gln
 210 215 220
 Ser Leu Lys Leu Leu Gly Glu Ile Leu Leu Asn Arg Ala Asn Arg Ser
 225 230 235 240
 Val Met Thr Arg Tyr Ile Ser Ser Ala Glu Asn Leu Lys Leu Met Met

				245					250					255			
Ile	Leu	Leu	Arg	Asp	Lys	Ser	Lys	Asn	Ile	Gln	Phe	Glu	Ala	Phe	His		
			260					265					270				
Val	Phe	Lys	Leu	Phe	Val	Ala	Asn	Pro	Glu	Lys	Ser	Glu	Glu	Val	Ile		
		275					280					285					
Glu	Ile	Leu	Arg	Arg	Asn	Lys	Ser	Lys	Leu	Ile	Ser	Tyr	Leu	Ser	Ala		
	290				295			300									
Phe	His	Thr	Asp	Arg	Lys	Asn	Asp	Glu	Gln	Phe	Asn	Asp	Glu	Arg	Ala		
305					310					315					320		
Phe	Val	Ile	Lys	Gln	Ile	Glu	Arg	Leu									
				325													

<210> SEQ ID NO 95

<211> LENGTH: 399

<212> TYPE: PRT

<213> ORGANISM: *Saccharomyces cerevisiae*

<400> SEQUENCE: 95

Met	Phe	Lys	Lys	Tyr	Lys	Asn	Gln	Asp	Leu	Asp	Met	Ala	Phe	Trp	Trp		
1				5				10						15			
Lys	Lys	Asn	Pro	Lys	Thr	Pro	Ser	Asp	Tyr	Ala	Arg	Leu	Ile	Ile	Glu		
		20					25					30					
Gln	Leu	Asn	Lys	Phe	Ser	Ser	Pro	Ser	Leu	Thr	Gln	Asp	Asn	Lys	Arg		
		35				40					45						
Lys	Val	Gln	Glu	Glu	Cys	Thr	Lys	Tyr	Leu	Ile	Gly	Thr	Lys	His	Phe		
	50				55			60									
Ile	Val	Gly	Asp	Thr	Asp	Pro	His	Pro	Thr	Pro	Glu	Ala	Ile	Asp	Glu		
65				70				75						80			
Leu	Tyr	Thr	Ala	Met	His	Arg	Ala	Asp	Val	Phe	Tyr	Glu	Leu	Leu	Leu		
			85				90						95				
His	Phe	Val	Asp	Leu	Glu	Phe	Glu	Ala	Arg	Arg	Glu	Cys	Met	Leu	Ile		
		100					105					110					
Phe	Ser	Ile	Cys	Leu	Gly	Tyr	Ser	Lys	Asp	Asn	Lys	Phe	Val	Thr	Val		
		115				120					125						
Asp	Tyr	Leu	Val	Ser	Gln	Pro	Lys	Thr	Ile	Ser	Leu	Met	Leu	Arg	Thr		
	130				135			140									
Ala	Glu	Val	Ala	Leu	Gln	Gln	Lys	Gly	Cys	Gln	Asp	Ile	Phe	Leu	Thr		
145				150				155						160			
Val	Gly	Asn	Met	Ile	Ile	Glu	Cys	Ile	Lys	Tyr	Glu	Gln	Leu	Cys	Arg		
		165				170						175					
Ile	Ile	Leu	Lys	Asp	Pro	Gln	Leu	Trp	Lys	Phe	Phe	Glu	Phe	Ala	Lys		
		180				185						190					
Leu	Gly	Asn	Phe	Glu	Ile	Ser	Thr	Glu	Ser	Leu	Gln	Ile	Leu	Ser	Ala		
	195				200						205						
Ala	Phe	Thr	Ala	His	Pro	Lys	Leu	Val	Ser	Lys	Glu	Phe	Phe	Ser	Asn		
	210			215				220									
Glu	Ile	Asn	Ile	Ile	Arg	Phe	Ile	Lys	Cys	Ile	Asn	Lys	Leu	Met	Ala		
225				230				235						240			
His	Gly	Ser	Tyr	Val	Thr	Lys	Arg	Gln	Ser	Thr	Lys	Leu	Leu	Ala	Ser		
		245				250						255					
Leu	Ile	Val	Ile	Arg	Ser	Asn	Asn	Ala	Leu	Met	Asn	Ile	Tyr	Ile	Asn		
	260					265						270					
Ser	Pro	Glu	Asn	Leu	Lys	Leu	Ile	Met	Thr	Leu	Met	Thr	Asp	Lys	Ser		
	275					280						285					
Lys	Asn	Leu	Gln	Leu	Glu	Ala	Phe	Asn	Val	Phe	Lys	Val	Met	Val	Ala		
	290				295			300									
Asn	Pro	Arg	Lys	Ser	Lys	Pro	Val	Phe	Asp	Ile	Leu	Val	Lys	Asn	Arg		
305				310				315						320			
Asp	Lys	Leu	Leu	Thr	Tyr	Phe	Lys	Thr	Phe	Gly	Leu	Asp	Ser	Gln	Asp		


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<210> SEQ ID NO 97
<211> LENGTH: 8
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: FLAG peptide
<400> SEQUENCE: 97
    Asp Tyr Lys Asp Asp Asp Lys
    1             5
<210> SEQ ID NO 98
<211> LENGTH: 15
<212> TYPE: PRT
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: Bovine MBP fragment
<400> SEQUENCE: 98
    Gly His His Ala Ala Arg Thr Thr His Tyr Gly Ser Leu Pro Gln
    1             5             10             15
<210> SEQ ID NO 99
<211> LENGTH: 73
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 99
    ggatccgccca ccattggagca gaagctgac tctgaagagg acttgccgtt cccgtttggg 60
    aagtctcaca aat 73
<210> SEQ ID NO 100
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 100
    ggatccttaa gcttcttgct gagctggctc ctcc 34
<210> SEQ ID NO 101
<211> LENGTH: 78
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 101
    caccggatcc gccaccatgg agcagaagct gatctctgaa gaggacttgc ctttggttag 60
    taaatcacac aaaaatcc 78
<210> SEQ ID NO 102
<211> LENGTH: 34
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 102
    ggatcctcaa ggggccgttt tcttcaagtc tcgg 34
<210> SEQ ID NO 103
<211> LENGTH: 69
<212> TYPE: DNA
<213> ORGANISM: Artificial

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<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 103
      ggatccgccca ccatgggacta caaggacgac gatgacaagt catttcttgt aagtaaacca      60
      gagcgaatc                                                                69
<210> SEQ ID NO 104
<211> LENGTH: 35
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR prime
<400> SEQUENCE: 104
      ggatcctcag aactcccaat cgtccacctc cagct                                35
<210> SEQ ID NO 105
<211> LENGTH: 68
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR prime
<400> SEQUENCE: 105
      ggatccgccca ccatgggacta caaggacgac gatgacaagt ctcttttggg ttgcttctgc      60
      acttcaag                                                                68
<210> SEQ ID NO 106
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 106
      ggatccctag aattcccagt atgagtcttt ttcacg                                36
<210> SEQ ID NO 107
<211> LENGTH: 66
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 107
      actagtgccca ccatgggacta caaggacgac gatgacaaga agctcatcgg caagtacctg      60
      atgggg                                                                66
<210> SEQ ID NO 108
<211> LENGTH: 36
<212> TYPE: DNA
<213> ORGANISM: Artificial
<220> FEATURE:
<223> OTHER INFORMATION: PCR primer
<400> SEQUENCE: 108
      actagttcag tcctccaggt agggcactac agtcat                                36
<210> SEQ ID NO 109
<211> LENGTH: 14
<212> TYPE: PRT
<213> ORGANISM: Homo sapiens
<400> SEQUENCE: 109
      Cys Asp Pro Met Lys Arg Ala Thr Ile Lys Asp Ile Arg Glu
      1                      5                      10
<210> SEQ ID NO 110
<211> LENGTH: 22
<212> TYPE: PRT

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<213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 110
 Leu Ser Asn Met Met Ser Asp Gly Glu Phe Leu Arg Thr Ser Cys Gly
 1 5 10 15
 Ser Pro Asn Arg Arg Arg
 20
 <210> SEQ ID NO 111
 <211> LENGTH: 13
 <212> TYPE: PRT
 <213> ORGANISM: Rattus rattus
 <400> SEQUENCE: 111
 Lys Phe Leu Arg Thr Ser Cys Gly Ser Pro Asn Tyr Ala
 1 5 10
 <210> SEQ ID NO 112
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 112
 actgcagccc tggagcccag gaagc 25
 <210> SEQ ID NO 113
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 113
 ctagttgagc ttgctgcaga tctccagcgc 30
 <210> SEQ ID NO 114
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 114
 actagtgccca ccatgtaccc atacgatgtg ccagattacg ccgaaggggc cgccgcgcct 60
 gtggcgggg 69
 <210> SEQ ID NO 115
 <211> LENGTH: 30
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 115
 ctagttgagc ttgctgcaga tctccagcgc 30
 <210> SEQ ID NO 116
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 116
 actagtgccca ccatgtaccc atacgatgtg ccagattacg ccgagtcgct ggttttcgcg 60
 cggcgcctcc 69
 <210> SEQ ID NO 117
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 117
 tcaggtgagc tttgagcaga ccctcagtgc ctg 33
 <210> SEQ ID NO 118
 <211> LENGTH: 55
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 118
 gcgtcgacta cccatacgat gtgccagatt acgccgtcat ggcggatggc ccgag 55

<210> SEQ ID NO 119
 <211> LENGTH: 55
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 119
 gcactagtta cccatacgat gtgccagatt acgccgtcat ggcggtatggc ccgag 55

<210> SEQ ID NO 120
 <211> LENGTH: 36
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 120
 gagcgggccgc taattcacca ggacataccc gttgtg 36

<210> SEQ ID NO 121
 <211> LENGTH: 60
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 121
 gcggatccta cccatacgat gtgccagatt acgccgttat catgtcggag ttcagcgcg 60

<210> SEQ ID NO 122
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 122
 gagcgggccgc tcaactgcacc aggacaaacy tgcc 34

<210> SEQ ID NO 123
 <211> LENGTH: 75
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 123
 gcggatccta cccatacgat gtgccagatt acgccaaga ttatgatgaa cttctcaaatt 60
 attatgaatt acatg 75

<210> SEQ ID NO 124
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 124
 gtgcggccgc ttataccttg cagctagata ggatgtcttc c 41

<210> SEQ ID NO 125
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 125
 ccacccccac ccaccccgac acgccaata tgtgggcccc tatcggtgg agaagacgct 60
 gggcaaaagg 69

<210> SEQ ID NO 126
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 126
 cgatgcagcc tctcgcggtc cctgaagcag c 31

<210> SEQ ID NO 127
 <211> LENGTH: 31
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 127
 gctgcttcag ggaccgagaggctgcac g 31

<210> SEQ ID NO 128

<211> LENGTH: 28
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 128
 tcagggcaga ggggtcccgt tgggtggcc 28
 <210> SEQ ID NO 129
 <211> LENGTH: 67
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 129
 ggtgggggct ctcccgccta ccacctcccc cacccccacc cccacccacc ccagcacgcc 60
 caatatg 67
 <210> SEQ ID NO 130
 <211> LENGTH: 76
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 130
 ggatcctacc catac gatgt gccagattac gcctcgtccg gggccaagga gggaggtggg 60
 ggtctctccc cctacc 76
 <210> SEQ ID NO 131
 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 131
 gcggatccta cccatacgat gtgcc 25
 <210> SEQ ID NO 132
 <211> LENGTH: 69
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 132
 ggatccgcc caatgtaccc atacgatgtg ccagattacg ccacatcgac ggggaaggac 60
 ggcggcgcg 69
 <210> SEQ ID NO 133
 <211> LENGTH: 57
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 133
 gcggccgctc agaggctact ctctagctg gtggccacct tctggccctt aagccca 57
 <210> SEQ ID NO 134
 <211> LENGTH: 90
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 134
 ggagccgggc ccgcgggccg cctgctgcct ccgccgcgc cgggggtcccc agccgcccc 60
 gctgccgtgt cccctgcggc cggccagccg 90
 <210> SEQ ID NO 135
 <211> LENGTH: 41
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 135
 tgaagaggtt actgaaacca aaatctgcta tttt gatatt c 41
 <210> SEQ ID NO 136
 <211> LENGTH: 87
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 136
 gattacgccg cggcgggcggc ggcgagcgga gctggcgggg ctgccggggc cgggactggg 60

ggagccgggc ccgcgggccg cctgctg 87
 <210> SEQ ID NO 137
 <211> LENGTH: 55
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 137
 gcggatccta cccatacgat gtgccagatt acgccgcggc ggcggcggcg agcgg 55
 <210> SEQ ID NO 138
 <211> LENGTH: 90
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 138
 atagcagatt ttggtttcag taacctcttc actcctgggc agctgctgaa gacctgggtg 60
 ggcagccctc cctatgctgc acctgaactc 90
 <210> SEQ ID NO 139
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 139
 ctgtggacat aaaaaatggg atgcggaact ttcc 34
 <210> SEQ ID NO 140
 <211> LENGTH: 34
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 140
 ggaaaagttcc gcatccatt ttttatgtcc acag 34
 <210> SEQ ID NO 141
 <211> LENGTH: 33
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 141
 gagcgccgc ttacacgcct gcctgctcca tgc 33
 <210> SEQ ID NO 142
 <211> LENGTH: 54
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 142
 gcgaattcta cccatacgat gtgccagatt acgcctcggc ccggacgcca ttgc 54
 <210> SEQ ID NO 143
 <211> LENGTH: 37
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 143
 catcatactt ctgatttatt aaggcatcat ttatttc 37
 <210> SEQ ID NO 144
 <211> LENGTH: 37
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 144
 gaaataaatg atgccttaat aaatcagaag tatgatg 37
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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 gagtcgactt acagcttaag ctcatttgct atttttgatg c 41
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 <213> ORGANISM: Homo sapiens
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 gagcggccgc ttacagctta agctcatttg ctatttttga tgc 43
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 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 gcgtcgacta cccatacgat gtgccagatt acgccattcg gggccgcaac tcagcc 56
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 <212> TYPE: DNA
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 <211> LENGTH: 73
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 gcggccgcag ccaccatgta cccatacgat gtgccagatt acgcctccac taggacccca 60
 ttgccaacgg tga 73
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 <213> ORGANISM: Homo sapiens
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 gcggccgcctt acagcttttag ctcatggga attttggaag c 41
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 <211> LENGTH: 68
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
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 gccccggg 68
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 <211> LENGTH: 25
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 154
 tgccctgaaa cagctccggg gcggc 25
 <210> SEQ ID NO 155
 <211> LENGTH: 25

<212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 155 25
 gggatcgaag ctggacacgt tctgc
 <210> SEQ ID NO 156
 <211> LENGTH: 39
 <212> TYPE: DNA
 <213> ORGANISM: Homo sapiens
 <400> SEQUENCE: 156 39
 ggggccgctc acactccagg ggaatcggag cagccgggg
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 <211> LENGTH: 15
 <212> TYPE: PRT
 <213> ORGANISM: Artificial
 <220> FEATURE:
 <223> OTHER INFORMATION: Artificial AMPK kinase substrate
 <400> SEQUENCE: 157
 Ala Met Ala Arg Ala Ala Ser Ala Ala Ala Leu Ala Arg Arg Arg
 1 5 10 15
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 <211> LENGTH: 23
 <212> TYPE: PRT
 <213> ORGANISM: Homo sapiens
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 Leu Ser Asn Leu Tyr His Gln Gly Lys Phe Leu Gln Thr Phe Cys Gly
 1 5 10 15
 Ser Pro Leu Tyr Arg Arg Arg
 20
 <210> SEQ ID NO 159
 <211> LENGTH: 377
 <212> TYPE: PRT
 <213> ORGANISM: Caenorhabditis elegans
 <400> SEQUENCE: 159
 Met Pro Leu Leu Phe Gly Lys Ser His Lys Ser Pro Ala Asp Val Val
 1 5 10 15
 Lys Thr Leu Arg Glu Val Leu Thr Ile Leu Asp Lys Leu Pro Pro Pro
 20 25 30
 Lys Leu Asp Lys Asp Gly Asn Ile Gln Ser Asp Lys Lys Tyr Asp Lys
 35 40 45
 Ala Leu Asp Glu Val Ser Lys Asn Val Ala Met Ile Lys Ser Phe Ile
 50 55 60
 Tyr Gly Asn Asp Ser Ala Glu Pro Ser Ser Glu His Val Val Gln Val
 65 70 75 80
 Ala Gln Leu Ala Gln Glu Val Tyr Asn Ala Asn Ile Leu Pro Met Leu
 85 90 95
 Ile Lys Met Leu Pro Lys Phe Glu Phe Glu Cys Lys Lys Asp Val Gly
 100 105 110
 Gln Ile Phe Asn Asn Leu Leu Arg Arg Gln Ile Gly Thr Arg Ser Pro
 115 120 125
 Thr Val Glu Tyr Leu Gly Ala Arg Pro Glu Ile Leu Ile Gln Leu Val
 130 135 140
 Gln Gly Tyr Ser Val Pro Asp Ile Ala Leu Thr Cys Gly Leu Met Leu
 145 150 155 160
 Arg Glu Ser Ile Arg His Asp His Leu Ala Lys Ile Ile Leu Tyr Ser
 165 170 175
 Asp Val Phe Tyr Thr Phe Phe Leu Tyr Val Gln Ser Glu Val Phe Asp
 180 185 190

